

WEST Search History

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DATE: Thursday, December 18, 2003

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT,PGPB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L10	(L8 and cre) and @pd > 20031218	0
<input type="checkbox"/>	L9	(L8 and L7) and @pd > 20031218	0
<input type="checkbox"/>	L8	(codon near3 mammal\$) and @pd > 20031218	0
<input type="checkbox"/>	L7	(cre recombinase) and @pd > 20031218	0
<input type="checkbox"/>	L6	(modif\$ near3 cre recombinase) and @pd > 20031218	0
<input type="checkbox"/>	L5	(L3 and cre) and @pd > 20030710	14
<input type="checkbox"/>	L4	(L3 and L2) and @pd > 20030710	7
<input type="checkbox"/>	L3	(codon near3 mammal\$) and @pd > 20030710	69
<input type="checkbox"/>	L2	(cre recombinase) and @pd > 20030710	445
<input type="checkbox"/>	L1	(modif\$ near3 cre recombinase) and @pd > 20030710	1

END OF SEARCH HISTORY



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

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110462

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

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Requester's Full Name: Celine Qian Examiner # 78710 Date: 12/15/03
 An Unit 1636 Phone Number 306-0283 Serial Number 091662128
 Mail Box and Bldg/Room Location: 11E012/11C10 Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Modified Cre-Recombinase Gene for MammalsInventors (please provide full names): Miyagawa et al.Earliest Priority Filing Date: 9/14/00

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for SEQ ID NO: 1

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # _____	AA Sequence (#) _____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel Orbit _____
Date Searcher Provided: <u>12/15/03</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>12/16/03</u>	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>01</u>
Client's Prep Time _____	Patent Family _____	WWW Internet _____
On Hold Time _____	Other _____	Other (specify) _____

PT 1000 12/15/03

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM nucleic - nucleic search, using sw model
Run on: December 16, 2003, 00:09:53 ; Search time 4150 Seconds
(without alignments)
10350.628 Million cell updates/sec

Title: US-09-662-128A-1
Perfect score: 1050
Sequence: 1 atgcccagaagaagaa.....gcctgctgagagagcgac 1050

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_of:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rtd:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1050	100.0	1050	6	E63780
2	755	71.9	2346	6	AR302443
3	754.4	71.8	1032	6	AR302441
4	727.4	69.3	1080	12	AY056050
5	672.6	64.1	1725	6	AX343224
6	672.6	64.1	1725	6	AX353872
7	672.6	64.1	1800	6	AX343226
8	672.6	64.1	1800	6	AX353874
9	639.4	60.9	4847	6	AX191674
10	639.4	60.9	4960	6	AX191663
11	639.4	60.9	5365	6	AX114854
12	633.2	60.3	5894	12	AF334827
13	630	60.0	5261	6	AR222049
14	630	60.0	5261	6	AX205077
15	618.4	58.9	1553	6	AX380948
16	618.4	58.9	1553	6	AX411030
17	618.4	58.9	1553	7	WYP1CRE
18	617.4	58.8	1032	6	AX343218
19	617.4	58.8	1032	6	AX348053
20	617.4	58.8	1032	6	AX353866
21	617.4	58.8	1032	6	AX353920
22	617.4	58.8	1074	6	AX150382
23	617.4	58.8	1074	6	AX191635
24	617.4	58.8	1623	6	AX191647
25	617.4	58.8	1740	6	AR067794
26	617.4	58.8	1983	6	AX411753
27	617.4	58.8	1983	6	AX411755
28	617.4	58.8	1983	6	AX411757
29	617.4	58.8	2004	6	A64972
30	617.4	58.8	2004	6	A64972
31	617.4	58.8	2004	6	AX150386
32	617.4	58.8	2055	6	AX191639
33	617.4	58.8	2346	6	AX191654
34	617.4	58.8	2346	6	AR302442
35	617.4	58.8	2346	6	AR302444
36	617.4	58.8	2346	6	AR302445
37	617.4	58.8	4488	6	AX191651
38	617.4	58.8	6094	6	A64973
39	616.8	58.7	6869	12	AF397196
40	616.8	58.7	6869	12	AF298789
41	616.8	58.7	6979	12	AF298780
42	616.8	58.7	7051	12	AF298782
43	616.6	58.7	4491	6	AF298785
44	616.6	58.7	4491	6	AR240211
45	615.8	58.6	1125	6	AX191652

ALIGNMENTS

RESULT 1

LOCUS	E63780	1050 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Mammal-type Cre recombinase gene.				
ACCESSION	E63780				
VERSION	E63780.1	GI:22553618			
KEYWORDS	JP 2001086989-A/1.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 1050)				
AUTHORS	Miyagawa,S. and Okabe,M.				
TITLE	Mammal-type Cre recombinase gene				
JOURNAL	Patent: JP 2001086989-A 1 03-APR-2001;				
	PRESIDENT OF OSAKA UNIVERSITY				

Qy 383 GCAAGGAGAACTGTGAACGCGGAGCGCCCAAGCAGCGCCCTGCGGCGCACGG 442
Db |||||
Qy 362 GGAAGGAAAAGTGTGATCGCGCGAAAGGCGAAGCAGGCGCTCGCTTGCAGAGGACG 421
Db |||||
Qy 443 ACTTCGACCAAGTGTGCGGACCTGTATGGAGAACAGCAGCGCTGCGCAGGACATCCGCAACC 502
Db |||||
Qy 422 ATTTTCGACCAAGTGTGCGGACCTGTATGGAGAACAGCAGCGCTGCGCAGGACATAGGAACC 481
Db |||||
Qy 503 TGGCCTTCTGGGATTCGCTTACAAACCTGTGCGGATCGCGGAGATCGCGCGCATCC 562
Db |||||
Qy 482 TGGCGTCTCTCGGAATTCATACAAACGCTCTCAGGATCGCGGAAATTCGCGCATTC 541
Db |||||
Qy 563 GCGTGAAGACATCAGCGCGACCGCGCGCGCGATGCTATCCACATCGCGCGCACCA 622
Db |||||
Qy 542 GCGTGAAGACATCAGCGCGACCGCGCGCGCGATGCTATCCACATTCGCGAGGACCA 601
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Qy 623 AGACCTCGGTGAGCAACCGCGCGCTGTGAGAGGCGCTGAGCGTGGCGGTGACCAAGCTGG 682
Db |||||
Qy 602 AGACGCTCGTTTCCACCGCAGCGGTGCGAAAGGCGCTCAGGCTCGGAGTGACCAAGCTCG 661
Db |||||
Qy 583 TGGAGCGTGTATCAGCGTGTGAGCGCGGTGGCGGACGACCGCCCAACCTACCTGTTCTGCC 742
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Db |||||
Qy 782 TGGAGGCTATTTTCGAGGCGCAACCGCGCGCTGATCTAGCGGCGCGCGCGCGCGCGCGCG 841
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Qy 842 AACGCTACTGCGATCTGTCGCGGCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 901
Db |||||
Qy 923 GCGCGCGGTGAGCATCCCGGAGATCATGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
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Qy 902 GCGCGCGGTGTTTCCATCCCGGAAATCATGCGAGCGCGGTGATGCGAACATTTG 961
Db |||||
Qy 983 TGATGAATCATCCGCAACCTGTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
Db |||||
Qy 962 TCATGAATCATTCGCAACCTTTCAGAGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1021
Db |||||

RESULT 3
AR302441
LOCUS AR302441 1032 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2 from patent US 6541231.
ACCESSION AR302441
VERSION AR302441.1 GI:31690708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Baszczynski,C.L., Iyznik,L.A., Gordon-Kamm,W.J., Guan,X., Rao,A.G. and Tgigliani,L.A.
TITLE Method for the integration of foreign DNA into eukaryotic genomes
JOURNAL Patent: US 6541231-A 2 01-APR-2003;
FEATURES
Location/Qualifiers
source 1..1032
BASE COUNT 228 a 326 c 301 g 177 t
ORIGIN
Query Match 71.8%; Score 754.4; DB 6; Length 1032;
Best Local Similarity 83.4%; Pred. No. 4.8e-68;

Matches 857; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
Qy 23 TGAGCAACCTGTCTGACCGTGCACAGAACTCTGCCCGCTTCCCGTGGAGCCCAACGACG 82
Db |||||
Qy 2 TGTCAAACCTGTCTCACCGTTCACCAAGAACTTCCGGCTCTTCCAGTGGACGCGACGTCG 61
Db |||||
Qy 83 ACAGAGTGGCGCAAGAACTGTATGGACATGTTTCCGGAGCCCGCAGGCTTTCAGCGAGACA 142
Db |||||
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Db |||||
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Qy 383 GCAAGGAGACGTGGAGCG 442
Db |||||
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Db |||||
Qy 443 ACTTCGACCAAGTGTGCGGACCTGTATGGAGAACAGCAGCGCTGCGCAGGACATCCGCAACC 502
Db |||||
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Db |||||
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Db |||||
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Db |||||
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Db |||||
Qy 623 AGACCTGTGTGAGCACCGCGCGGTGTGAGAGGCGCTGAGCGCTGGGCGTGTGACCAAGCTGG 682
Db |||||
Qy 602 AGACGCTCGTTTCCACCGCAGCGGTTCGAAAGGCGCTCAGGCTCGGAGTGACCAAGCTCG 661
Db |||||
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Db |||||
Qy 662 TCGAACGCTGATCTCGTGTGCGGCTCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 721
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Qy 863 AGCGCTACTGCGCTGTGAGCGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 922
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Qy 1022 ATGCTGAC 1029
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RESULT 4	AY056050	1080 bp	DNA	linear	SYN 19-NOV-2001
LOCUS	AY056050	Synthetic construct codon-optimized cre recombinase (iCre) gene, complete cds.			
DEFINITION	AY056050				
ACCESSION	AY056050.1	GI:17016299			
VERSION					
KEYWORDS		synthetic construct			
SOURCE		synthetic construct			
ORGANISM		artificial sequences.			
REFERENCE		1 (bases 1 to 1080)			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.				
TITLE	Codon-Optimized Cre Recombinase Expression in the Mouse				
JOURNAL	Unpublished				
REFERENCE		2 (bases 1 to 1080)			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-SEP-2001) Molecular Neurobiology, Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany				
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		/db_xref="taxon:32630"			
		/note="derived from bacteriophage P1"			
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CDS	14..1069	/gene="iCre"			
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BASE COUNT	248 a 294 c 319 g 219 t				
ORIGIN		Query Match 69.3%; Score 727.4; DB 12; Length 1080; Best Local Similarity 80.8%; Pred. No. 2.6e-65; Matches 848; Conservative 0; Mismatches 201; Indels 0; Gaps 0;			
Qy	2	TGCCCAAGAGAGAGAGGTGACAACTGCTGACCGTGACACAGAACCTGCGCGCCC	61		
Db	18	TGCCCAAGAGAGAGAGGTGACAACTGCTGACCGTGACACAGAACCTGCGCGCCC	77		
Qy	62	TGCCCGTGAGCGCCACGACGAGTGGCGCAAGACCTGATGACATGTTCCCGGACC	121		
Db	78	TCCCTGTGATGCCACCTCTGATGAAGTCAGGAAGAACCTGATGACATGTTCAAGGACA	137		
Qy	122	GCCAGGCTTTCAGCGAGACACACCTGGAAAGATGCTGCTGAGCGTGTGCGCAGCTGGGCGC	181		
Db	138	GCCAGGCTTTCAGCGAGACACACCTGGAAAGATGCTGCTGCTGTGTGACATGCTGGGCTG	197		
Qy	182	CTGTGTGAAGTGAACACCGAAGTGGTTCCCGCGGACCGCGAGACGTCGCGGACT	241		
Db	198	CTGTGTGAAGTGAACACCGAAGTGGTTCCCGCGGACCGCGAGACGTCGCGGACT	257		

Qy	242	ACCTGCTGTACCTCGAGGCGCGCGCTGCGCGTGAAGACCATTCAGCAGACCTGGGCC	301		
Db	258	ACCTCCTGTACCTGCAAGCCAGAGCGCTGGCTGTGAAGACCATTCAGCAGACCTGGGCC	317		
Qy	302	AGCTGAACATCTGCACCGCGCAGCGCGCTGCGCGCCCGCAGCAGCAGCAACCCGTGA	361		
Db	318	AGCTCAACATGCTGCACAGGAGATCTGGCTGCTGCGCCCTTCTGATCTCCAATGCTGTGT	377		
Qy	362	GCCTGTGATGCGCGCGCATCCGCAAGGAGAACGTGGACGCGCGGAGCGCGCCCAAGCAGG	421		
Db	378	CCCTGTGATGAGGAGAAATCAGAAAGGAGAAATGTGGATGCTGGGGAGAGAGCCCAAGCAGG	437		
Qy	422	CCCTGGCTTCGAGGCGACCGACTTCGACCAAGTGGCGCAGCTGATGAGAACAGCGACC	481		
Db	438	CCCTGGCTTCGAGGCGACCGACTTCGACCAAGTGGCGCAGCTGATGATGAGAACCTTGACA	497		
Qy	482	GCTGCCAGGACATCCGCAACCTGCGCTTCTGCGGCATCGCTACAAACCTGCTGCGCA	541		
Db	498	GATGCCAGGACATCAGGAACCTGCGCTTCTGCGGCATGCTTACAAACCTGCTGCGCA	557		
Qy	542	TCGCGGAGATGCGCGCGCATCCGCTGAAGGACATCAGCCGACCGAGCGCGCGCATGC	601		
Db	558	TGCGCGAAATTCGCGGAAATCAGAGTGAAGGACATCTCCCGCAGCATGGTGGGAGAAATGC	617		
Qy	602	TGATCCACATCGCGCGCACCAAGACCTGCTGAGCAGCGCGCGGCTGAGAGAGCCCTGA	661		
Db	618	TGATCCACATTCGCGGACCAAGACCTGCTGAGCAGCGCGCGGCTGAGAGAGCCCTGT	677		
Qy	662	GCCTGGGCGTGACCAAGCTGTGGAGCGCTGGATCAGCTGAGCGGCTGGCGCGACGACC	721		
Db	678	CCCTGGGCGTTACCAAGCTGTGGAGAGATGGATCTCTGTGCTGTGTGCTGATGACC	737		
Qy	722	CCAAACAATCTGCTTCTGCGCGTGGCGAAGAACGGCGTGGCGCGCCCGCAGCGCCACCA	781		
Db	738	CCAAACAATCTGCTTCTGCGCGTGGCGAAGAACGGCGTGGCGCGCCCGCAGCGCCACCT	797		
Qy	782	GCCAGCTGAGCACCGCGCGCTGAGGCGCATCTTCGAGGCGCACCCACCGCTGATCAG	841		
Db	798	CCCAACTGTCCACCGCGCGCTGGAAAGGATCTTTGAGGCGCACCCACCGCTGATCTATG	857		
Qy	842	GCGCAAGGACGACAGCGCGCGCTACCTGCGCTGGAGCGGCACAGCGCGCGCGTGG	901		
Db	858	GTGCCAAGGATGATCTTGGCGAGAGATACCTGGGCTGCTGGCCATCTGCCAGAGTGG	917		
Qy	902	GCGCGCGCGCGACATGCGCGCGCGCGCGCTGAGCATCCCGGAGATCATGAGCGCGCGCG	961		
Db	918	GTGCTGCGCAGGACATGCGCGCGCGCGCTGCTGCTCCATCCCTGAAATCATGCGAGCTGGTG	977		
Qy	962	GCTGACCAACGCTGAAACATGCTGATGATGATACATCCGCAACCTGAGCAGCGAGACCGCGG	1021		
Db	978	GCTGACCAACGCTGAAACATGATGATGATGATACATCAGAAACCTGAGACTCTGAGACTGGGG	1037		
Qy	1022	CCATGCTGCGCTGCTGGAGGACGGCGAC	1050		
Db	1038	CCATGCTGAGGCTGCTCGAGGATGGGAC	1066		

RESULT 5	AX343224	1725 bp	DNA	linear	PAT 01-FEB-2002
LOCUS	AX343224	Sequence 7 from Patent EP1170364.			
DEFINITION	AX343224				
ACCESSION	AX343224.1	GI:18491580			
VERSION					
KEYWORDS		synthetic construct			
SOURCE		synthetic construct			
ORGANISM		artificial sequences.			
REFERENCE		1			
AUTHORS	Edenhofer,F.O., Wunderlich,T. and Rajewsky,K.				
TITLE	Mutations of cryptic splice sites in cre and cre-fusion proteins to improve the expression in inducibility				
JOURNAL	Patent: EP 1170364-A 7 09-JAN-2002; ARTEMIS Pharmaceuticals GmbH (DE)				

FEATURES	source	Location/Qualifiers	
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Best Local Similarity 80.3%; Pred. No. 8.2e-60;			
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QY	128	CCTTTACGCGAGCACACTCGAAGATGCTGCTGAGCGTGTGCGCAGCTGGCGCCCTGCT 187	
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QY	488	AGGACATCCGCAACCTGGCCCTTCTGGGCATGCTCTACCAACACCTCTGCGCATGCCG 547	
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QY	548	AGATCGCCCGCATCCGCGGTGAAGGACATCAGCCGCGCAGCGCGCGCGCGCATGCTATCC 607	
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RESULT 7
AX343226
LOCUS AX343226 1800 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 9 from Patent EP1170364.
ACCESSION AX343226

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VERSION AX343226.1 GI:18491582
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences
REFERENCE 1
AUTHORS Edenhofer, F.O., Wunderlich, T. and Rajewsky, K.
TITLE Mutations of cryptic splice sites in cre and cre-fusion proteins to improve the expression in inducibility
JOURNAL Patent: EP 1170364-A 9 09-JAN-2002; ARTEMIS Pharmaceuticals GmbH (DE)
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BASE COUNT 457 a 439 c 470 g 434 t
ORIGIN
Query Match 64.1%; Score 672.6; DB 6; Length 1800;
Best Local Similarity 80.3%; Pred. No. 8e-60;
Matches 789; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
QY 68 TGGACGCGCACCGAGCGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACCGCCAGG 127
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LOCUS AX191674 4847 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 40 from Patent WO0149832.
ACCESSION AX191674
VERSION AX191674.1 GI:15209855
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schwenk, F.
TITLE Transduction of recombinases for inducible gene targeting
JOURNAL Patent: WO 0149832-A 40 12-JUL-2001;
ARTEMIS Pharmaceuticals GmbH (DE)
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Query Match 60.9%; Score 639.4; DB 6; Length 4847;
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Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

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Db 3795 GCAATGGTGCCTGCTGGAAGATGGCA 3823

RESULT 10
AX191663
LOCUS AX191663 4960 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 29 from Patent WO0149832.
ACCESSION AX191663
VERSION AX191663.1 GI:15209844
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Schwenk, F.
TITLE Transduction of recombinases for inducible gene targeting
JOURNAL Patent: WO 0149832-A 29 12-JUL-2001;
ARTEMIS Pharmaceuticals GmbH (DE)
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Query Match 60.9%; Score 639.4; DB 6; Length 4960;
Best Local Similarity 75.6%; Pred. No. 1.3e-56;
Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

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LOCUS
DEFINITION Cloning vector pTurbo-Cre, 5894 bp DNA circular SYN 19-NOV-2002
AF334827
VERSION AF334827.1 GI:12965137
KEYWORDS
SOURCE
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Cloning vector pTurbo-Cre
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artificial sequences; vectors.
1 (bases 1 to 5894)
AUTHORS Lu,Z.H., Graubert,T.A. and Ley,T.J.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-2001) Division of Oncology, Section of Stem Cell
Biology, Washington University School of Medicine, 660 South Euclid
Avenue, Campus Box 8007, St. Louis, MO 63110-1093, USA

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Query Match 60.3%; Score 633.2; DB 12; Length 5894;
Best Local Similarity 75.3%; Pred. No. 5.4e-56;
Matches 788; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

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RESULT 13
LOCUS AR222049 5261 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6429001.
ACCESSION AR222049
VERSION AR222049.1 GI:23329405
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 5261)
AUTHORS Hardy,S.F.
TITLE Recombinant AAV packaging systems
JOURNAL Patent: US 6429001-A 7 06-AUG-2002;
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AUTHORS Hardy,S.F.
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    Matches 786; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 4 CCCAAGAAGAAGAGAGGTGAGCAACCTGTCGACCGTGACCAAGAACCTGCCCGCCCTG 63
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VERSION AX380948.1 GI:19575790
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
P1-like viruses.
REFERENCE 1

Li, Y., O'Donnell, C. P., Duan, H., Wu, Y. H. and Mcavoy, R.
Methods for the controlled, automatic excision of heterologous dna
from transgenic plants and dna-excising gene cassettes for use
therein
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Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	639.4	60.9	4847	22	His6-NLS-Cre-MTS f
6	639.4	60.9	4960	22	pGR-cre-pA vector
7	639.4	60.9	4960	22	pCMV-I-Cre-pA vect
8	639.4	60.9	4960	24	Recombinase domain
					Retroviral vector

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ALIGNMENTS

RESULT 1
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XX AC AAH41175;
XX DT 23-AUG-2001 (first entry)
XX DE Mammalian Cre recombinase gene.
XX KW Mammalian; Cre recombinase; organ transplantation; gene therapy;
XX KW animal disease model; ds.
XX OS Mammalia.
XX FN JP2001086989-A.
XX PD 03-APR-2001.
XX PF 17-SEP-1999; 99JP-0264364.
XX PR 17-SEP-1999; 99JP-0264364.
XX PA (OSAU) UNIV OSAKA.
XX DR WPI; 2001-360321/38.
XX DR P-PSDB; AAB98695.
XX PT Mammalian type Cre recombinase gene modified so as to have a high
PT expression efficiency in a mammal by selecting a codon of high
PT frequency for use in the mammal for expressing Cre recombinase -

CC constructing stably transformed eukaryotic cells, preferably plant
CC cells. The present sequence is a chimeric recombinase DNA encoding
CC mCre:FLPm, Cre protein from Bacteriophage P1 and FLP from
CC Saccharomyces, both maize preferred codons.

Sequence 2346 BP; 534 A; 807 C; 599 G; 406 T; 0 other;

Query Match 71.9%; Score 755; DB 22; Length 2346;
Best Local Similarity 83.4%; Pred. No. 3.2e-102;
Matches 857; Conservative 0; Mismatches 170; Indels 0

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Db	842	AACGCTACTCGCATGGTTCGCGGCACTCCGCGCGCTTGAGCTGCTAGGACATGGGCC	901
QY	923	GGCGCGGCTGAGCATCCCGAGATCATTCGAGGCGCGCGCTGGACCAACGTTGAACATCG	982

Db 902 GGGCGGGTGTTCATCCCGAAATCATGCGAGCGGGTGGATGACGAACGTGCAACATTG 961
 QY 983 TCATGAACATACATCCGCAACCTGCACAGCGAGACCGCGCATGGTGCCTGTGTGGAG 1042
 Db 962 TCATGAACATACATTGCAACCTTGACAGCGAGACCGCGCAATGGTTCGCTCTCTGGAAG 1021
 QY 1043 ACGGCGA 1049
 Db 1022 ATGGCGA 1028
 RESULT 3
 AAD10215
 ID AAD10215 standard; DNA; 1032 BP.
 XX AC AAD10215;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Chimeric moCRE recombinase DNA.
 XX
 KW Maize; site specific recombinase; expression cassette; chimeric; moCRE;
 KW Cre protein; ds.
 XX
 OS Chimeric - Zea mays.
 OS Chimeric - Bacteriophage P1.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1032
 FT /*tag= a
 FT /*product= "Chimeric moCRE protein"
 XX
 FN US6262341-B1.
 PD 17-JUL-2001.
 XX
 PF 17-NOV-1998; 98US-0193503.
 XX
 PR 18-NOV-1997; 97US-0065613.
 PR 18-NOV-1997; 97US-0065627.
 PR 08-SEP-1998; 98US-0099435.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Baszczynski CL, Lyznik LA, Gordon-Kamm WJ, Guan X, Rao AG;
 PI Tagliani LA;
 XX
 DR WPI; 2001-450495/48.
 DR P-PSDB; AAE05410.
 XX
 PT Integrating DNA of interest into genome of eukaryotic cell, by
 PT transforming plant cell with transfer cassette comprising DNA flanked
 PT by target sites for site-specific recombinases and providing
 PT recombinases in cell -
 XX
 PS Disclosure; Column 15-16; 30pp; English.
 XX
 CC The invention relates to compositions and methods for introducing
 CC a DNA of interest into a genomic target site. The methods and
 CC compositions involve the use of a combination of target sites for two
 CC site specific recombinases and expression of a chimeric recombinase
 CC with dual target site specificity. The compositions comprise novel
 CC site-specific recombinases with specificities to multiple target sites,
 CC and nucleotide sequences and expression cassettes encoding these
 CC recombinases or target sites. The method of integrating the foreign DNA
 CC into genome of eukaryotic cell involves transforming the cell having
 CC target sites for the novel recombinase with a DNA of interest that is
 CC flanked by corresponding target sites. The method is useful for
 CC constructing stably transformed eukaryotic cells, preferably plant
 CC cells. The present sequence is a chimeric recombinase DNA encoding
 CC moCRE. Cre protein from Bacteriophage P1 with maize preferred codons.
 XX
 SQ Sequence 1032 BP; 228 A; 326 C; 301G; 177 T; 0 other:

Query Match	71.8%;	Score 754.4;	DB 22;	Length 1032;
Best Local Similarity	83.4%;	Pred. No. 4.2e-102;		
Matches	857;	Conservative 0;	Mismatches 171;	Indels 0;
QY	23	TGAGCAACCTGCTGACCGTGCAACAGAACCTGCCGCCCTGCGTGGAGCGCCACCGG	82	
Db	2	TGTCCAAACCTGCTCAGCGTTCCACAGAACCTTCCGGGCTCTTCCAGTGGACCGCAGCTCG	61	
QY	83	ACGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCGACGCGCTTCAGCGAGCACA	142	
Db	62	ATGAGTCAGAGAAAGAACCTCATGACATGTTCCGCGACAGCAAGCGTTCAAGCGAGCACA	121	
QY	143	CCTGGAAAGATGCTGCTGAGCGTGTGCGCGACGTGGCGCGCTGGTGAAGCTGAACACCC	202	
Db	122	CCTGGAAAGATGCTGCTCTCCGTTCCGCGCTCTCTGGGCTGCAATGTCGAAGCTGAACACA	181	
QY	203	GCAAGTGGTTCCCGCGGAGCGCCGAGAGAGCTGCGGCACTACTGCTGTACCTGCAAGGCC	262	
Db	182	GGAAAGTGGTTCCCGCGCTGAGCCCGAGGACGTGAGGGATTACCTTCTGTACCTGCAAGCTC	241	
QY	263	GCGGCTTGGCGGTGAAGAACCATCAGACGACACTGGGCCAGCTGAAACATGCTGCACGCC	322	
Db	242	GCGGGCTGGCGAGTGAAGACCATCAGACACACTTGGACACTGAAATGCTTCACAGGC	301	
QY	323	GCAGCGCTTCCCGCGCCCGACAGCACAGCAACGCGGTGAGCGCTGGTATGCGCGCGCATCC	382	
Db	302	GCTCCGGCTTCCCGCGCCCGACGACTCGAACGCGGTGAGCTCGTATGCGCGCATCA	361	
QY	383	GCAAGGAGAACGTGAGCGCGGAGCGCGCAAGAGAGGCCCTGGCCTTGGAGCGCACCG	442	
Db	362	GGAAAGGAAACGTGATGCGCGCGAAAGGGCAAGACAGGCCCTCGCGTTCGAGAGGACCG	421	
QY	443	ACTTCGACCAAGTGGCGAGCCTGATGAGAACAGCGACCGCTGCCAGGACATCGCGACCC	502	
Db	422	ATTTGACCAAGTCCGAGCCTGATGAGAAACAGCAGAGTGCAGGACATTAGGACCC	481	
QY	503	TGGCCTTCTGGGCATCGCCTACAAACCTGCTGCGCATCGCCGAGATCGCCGCGATCC	562	
Db	482	TGGCGTTCTCGGAATTGCTATACAAACGCTCTCAGGATCGCGAAATTCGCCGCGATTC	541	
QY	563	GGGTGAAGGACATCAGCGGACCGACCGCGCGCGCATCTGTCATCCACATCGCGCGCACCA	622	
Db	542	GGGTGAAGGACATTAGCGGACCGACCGCGCGCAGATGCTTATCCACATTGGCGAGGACCA	601	
QY	623	AGACCTGTGTGACACCGCGGCTGGAGAGGCGCTGAGCCTGGGCGTGACCAAGCTGG	682	
Db	602	AGAGCTCTGTTTCACCGAGGGGTGCAAGAGGCCCTAGCCTCGGAGTGACCAAGCTCG	661	
QY	683	TGAGCGCTGGATCAGCGTGAGCGGCTGGCGGACGACCCCAACAACTACTCTGTTCTGCC	742	
Db	662	TCGAAACGCTGGAATCTCGTGTTCGGCGTTCGGGACGACCCCAACATCTCTTCTTGCC	721	
QY	743	GGGTGCGCAAGACGGGTGGCGCCCGCCAGCGCCACCAAGCAGCTGAGCACCGCGGCC	802	
Db	722	GGGTTCGCAAGAACGGGTTGGCTGCCCTTAGCGCCAACAGCAACTCAGCACGAGGGCCT	781	
QY	803	TGAGGGGATCTTCAGGGCCACCAACGCGCTGATCTACGGGCGCCAAAGACGAGCGGCC	862	
Db	782	TGGAAGGTATTTTGGAGGCCCAACACGCGCTGATCTACGGCGCGAAGGATGACAGCGGTC	841	
QY	863	AGCGCTACCTGGCTGGAGCGGCCACAGCGCCGCGTGGCGCGCGCGGACATGGCCC	922	
Db	842	AACGCTACCTCGCATGTTCCGGGCATCTCCGCCCGGTTGGAGCTGTAGGGACATGGCCC	901	
QY	923	GCGCGGCGGTGAGCATCCCGAGATCATGAGGCGGGCGGCTGGACCAACGTGAACATCG	982	
Db	902	GCGCGGCTGTTTCCATCCCGGAATCATGCGGCGGGTGGATGACCGAAGCTGAACATTG	961	
QY	983	TGATGAACATACCCGAAACCTGGAACAGCGAGACCGCGGCGAATGGTGCCTGCTGAGG	1042	
Db	962	TCATGAACATCATTCGCAACCTTCACAGCGAGACGGCGCAATGGTTCCGCTCTCTGAAG	1021	

Qy	1043	ACGGCGAC 1050	
Db	1022	ATGTCGAC 1029	
RESULT 4			
	AAAD35273		
ID	AAAD35273	standard; DNA; 1158 BP.	
XX	AAAD35273;		
XX			
DT	25-JUL-2002	(first entry)	
XX			
DE	His6-NLS-Cre-MTS fusion DNA.		
XX			
KW	Site-specific DNA recombinase; DRI; membrane translocation sequence; MTS;		
KW	cell-permeable recombinase; nuclear localisation signal; NLS; excretion;		
KW	trafficking; blood-brain barrier; His6-NLS-Cre-MTS fusion gene; chimeric;		
KW	simian virus 40; SV40; gene; ds.		
XX			
OS	Chimeric - Rhesus macaque polyoma virus.		
OS	Chimeric - Bacteriophage P1.		
OS	Chimeric - Unidentified.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..1158	
FT		/*tag= a	
FT		/product= "His6-NLS-Cre-MTS fusion protein"	
FT		/transl_except= (pos: 1153..1155, aa:Pro-Glx)	
XX			
PN	WO2002020737-A2.		
XX			
PD	14-MAR-2002.		
XX			
PF	07-SEP-2001; 2001WO-US28209.		
XX			
PR	07-SEP-2000; 2000US-230690P.		
XX			
PA	(UVA-) UNIV VANDERBILT.		
XX			
PI	Ruley HE, Jo D;		
XX			
DR	WPI; 2002-362248/39.		
XX	P-PSDB; AAE22205.		
DR			
XX			
PT	New isolated polypeptide comprising a cell-permeable site-specific DNA		
PT	recombinase and membrane translocation sequence for stimulating		
PT	site-specific DNA recombination in a cell		
XX			
PS	Claim 30; Page 42; 70bp; English.		

Query Match 60.9%; Score 639.4; DB 24; Length 1158;


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Db 3015 TATCTTCTATATCTTTCAGGCGCGGTCTGCAGCTAAATACTATCCAGCAACATTTGGGC 3074
Qy 301 CAGCTGAACATGCTGCAACCGCCGAGCGGCTGCCCCGCCAGCAGCAACAGCCCGTG 360
Db 3075 CAGCTAAACATGCTTCACTGCTGCTGCGGTGCGACAGCAAGTACAGCAATGCTGTT 3134
Qy 361 AGCTGTGTGATGCGCCGATCCGCAAGAGAACCTGGACGCGCGGAGCGGCCAAGCAG 420
Db 3135 TCACGTGTTATGCGCGGATCCGAAAGAAACCTTTGATGCGGTGAACGTGCAAAACAG 3194
Qy 421 GCCCTGGCTTCGAGCGCACCGACTTCGACCAAGTGGCGAGCTGATGGAGAACAGCAG 480
Db 3195 GCTCTAGGTTGCAAGCACTGATTCGACCAAGTTCGTTCACTCATGGAAATAGCGAT 3254
Qy 481 CGCTGCAGGACATCCGCAACCTGGCTTCTTGGGCTATCGCTTCAACACCTGCTGCGC 540
Db 3255 CGCTGCCAGGATATACGTAATCTGCAATTTCTGGGGATTGCTTATAACACCTGTTAGT 3314
Qy 541 ATCGCCGAGATCGCCGATCCGCTGAGGACATCAGCCGACCGGCGGCGCGCATG 600
Db 3315 ATAGCCGAAATGCGCAGATCAGGTTAAAGATATCTACGTACTGACGTTGGGAGATG 3374
Qy 601 CTGATCCACATCGCCGCGCACCAAGACCTGCTGAGCACCGCGCGTGGAGAGGCCCTG 660
Db 3375 TTAATCCATATTGCGAGAACGAAACGCTGTTAGCACCGCAGGTGAGAGAGCCACTT 3434
Qy 661 AGCTGGGCGTGACCAAGCTGCTGAGCGCTGAGATCAGCGTGAAGCGCGTGGCGCAGC 720
Db 3435 AGCTGGGGGTAACTAAACTGCTGAGCGATGGATTTCCGCTCTCTGCTGATGATGAT 3494
Qy 721 CCCAAACATACCTGTTCTGCGCGTGGCGAAGAACGCGTGGCGGCCGCCAGCCACC 780
Db 3495 CCGAATAACTACCTGTTTTCGCGGTGAGAAATAATGTTGCGCGCATCTGCCACC 3554
Qy 781 AGCCAGTGAACACCGCGCTGAGGAGCATCTTCGAGGCGCACCCACCGCTGATCTAC 840
Db 3555 AGCCAGCTATCACTCGCGCTGGAAGGGATTTTGAAGCAACTCATGATTGATTAC 3614
Qy 841 GCGCCCAAGACGACAGCGCCAGCTGCTGCTGCTGAGCGGCGCACAGCGCCGCTG 900
Db 3615 GCGCTAAGGATGACTCTGCTGCTGAGATACCTGCGCTGCTGAGCACAGTGCCTGTC 3674
Qy 901 GCGCCCGCGCAGATGCGCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGC 960
Db 3675 GGAGCCCGCGAGATATGGCCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGT 3734
Qy 961 GGCTGGACCAACGTAATGATGATGAATACATCCGCAACCTGGACAGCAGACCGCGC 1020
Db 3735 GGCTGGACCAATGTAATATTGTCATGAACCTATATCCGTAACCTGGATAGTGAAACAGG 3794
Qy 1021 GCCATGCTGCGCTGCTGGAGGACGGCGA 1049
Db 3795 GCAATGCTGCGCTGCTGGAGATGGCGA 3823
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RESULT 6

AAD09269

ID AAD09269 standard; DNA; 4960 BP.

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

XX AD09269;

XX AC

PD

XX 12-JUL-2001.

PF

XX 05-JAN-2001; 2001WO-EP00060.

PR

XX 07-JAN-2000; 2000EP-0100351.

PR

XX 10-NOV-2000; 2000EP-0124595.

XX

XX (ARTE-) ARTEMIS PHARM GMBH.

XX

XX Schwenk F;

PI

XX WPI; 2001-441873/47.

DR

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Query Match 60.9%; Score 639.4; DB 22; Length 4960;
Best Local Similarity 75.8%; Pred. No. 2.3e-85;
Matches 799; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 1 ATGCCCAAGAGAGAGAGGTGAGCAACCTCTGACCGTGACCAAGACCTGCGCGCC 60
Db 977 ATGCCCAAGAGAGAGAGGTGAGCAACCTCTGACCGTGACCAAGACCTGCGCGCC 1036

Qy 61 CTCCCGTGAOCCTCCAGCAGAGGTGCGCAAGAACCTGATGACATGTTCCGCGAC 120
Db 1037 TTACCGGTGATGCAACGAGTGTAGGTGCGCAAGAACCTGATGACATGTTCCGCGAC 1096

Qy 121 CGCAGCGCTTCAGCAGCAGCAGCTGGAAGATGCTCTGAGCGTGTGCGCAGCTGGCC 180
Db 1097 CGCAGCGGTTCCTGAGCATACCTGCAAAATGCTTCTGCTCGTTTTCGCGTGTGGCG 1156

Qy 181 GCCTGTGCAAGCTGAACCAACCGCAAGTGTTCCTCCGCGAGCCCGCAGCAGCTGCGCGAC 240
Db 1157 GCATGTGCAAGTGTGAATACCGGAATGTTTCCCGCAGAACCTGAGATGTTCCGAT 1216

Qy 241 TACCTGCTGATCCTGAGCGCCCGCGCTGCGCGTGAAGACCATCCAGCAGCACCTGGGC 300
Db 1217 TATCTTCTATCTTCAGCGCGCGTCTGGCAGTAAATACTATCCAGCAACATTTGGGC 1276

Qy 301 CAGCTGAACATGCTGACCGCGCAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 1277 CAGCTAAACATGCTTCATCGTCCGCGCTGCCACGACCAAGTACAGCAATGCTGTT 1336

Qy 361 AGCTGTGTGATGCGCGCATCCGCAAGAGAACCTGAGCGCGCGCGCGCGCGCGCGCGCG 420
Db 1337 TCATGTTATGCGCGGATCCGAAAGAAAGCTTGATGCGCGTGAAGCTGCAAAACAG 1396

Qy 421 GCCCTGGCTTCAGCGCACCGACTTCGACCAAGTTCGCGAGCGCGCGCGCGCGCGCGCG 480
Db 1397 GCTTAGCGTTCGACGCACTGATTCGACCAAGTTCGTTCTACTCATGAAAATAGCGAT 1456

Qy 481 CGCTGCCAGGACATCGCAACCTGCGCTTCCTGGGCGATCGCTTACAGCAACCTGCTGGC 540
Db 1457 CGCTGCCAGGATATCGTAATCTGCAATTTCTGGGGAATGCTTATTAACACCTGTTACGT 1516

Qy 541 ATCGCCGAGATCGCCGCGCATCCGCGTGAAGGACATCAGCGCGCACCGCGCGCGCGCG 600
Db 1517 ATAGCCGAAATTCGCAAGGATCAGGGTTAAGATATCTCAGTACTGCGTGGGAGATG 1576

Using site-specific DNA recombinase domain/protein transduction domain
fusion proteins for inducing target gene alterations in organisms or
cell cultures -

Example; Page 62-63; 85pp; English.

The present invention relates to use of fusion proteins comprising
a site-specific DNA recombinase domain e.g. Cre and a protein
transduction domain (PTD) e.g. the Human immunodeficiency virus
(HIV) derived TAR peptide, for preparing an agent for inducing
target gene alterations in a living organism or cell culture. The
present invention also provides a method for inducing gene
alterations in living organisms using the fusion proteins of the
invention. The present sequence is a pCMV-I-Cre-pA vector DNA.

QY 601 CTGATCCATCGGCCCCCAACAAGACCTCGTGGAGCAACCCCGCGCTGGAGAGGCGCTG 660
 Db |||||
 QY 1577 TTAATCCATATTGGCAGAACGAAACCGTGGTTAGCACCGCAGGTGTAGAGAGGCACCT 1636
 Db |||||
 QY 661 AGCTGGGCTGACCAAGCTGGTGGAGCGCTGGATCAGCGTGAGCGCGTGGCGGACG 720
 Db |||||
 QY 1637 AGCTGGGGTAACCTAAACTGGTGGAGCGATGATTTCCGTCTCTGGTGTAGCTGATG 1696
 Db |||||
 QY 721 CCCAACAACTACCTGTTCTCGCGGTGCGCAAGAACGGCGTGGCGCCGCCAGCGCAC 780
 Lb |||||
 QY 1697 CCGAATAACTACCTGTTTTCGCGGTGCGAAGAAATGTTGTCGCGGCCATCTGCACC 1756
 QY 781 AGCCAGCTGAGCACCCGGGCCCTGGAGGGCATCTTGAGGCCACCCACCGCCCTGATCTAC 840
 Db |||||
 QY 1757 AGCCAGCTATCAACTCGCGCCCTGGAAGGATTTTGAAGCAACTCATCGATTGATTTAC 1816
 QY 841 GGGCCCAAGACGACGCGCGAGCTACCTGCGCTGGAGCGGCCACAGCGCCCGGTG 900
 Db |||||
 QY 1817 GGGCGTAAAGATGACTCTGTGAGAGATACCTGCGCTGGTCTGGACACAGTGGCCGTG 1876
 QY 901 GGGCGCCCGCGACATCGGCCCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGG 960
 Db |||||
 QY 1877 GAGCGCGCGAGATATGGCCGCGCTGGAATTTCAATACCGGAGATCATGCAAGCTGG 1936
 QY 961 GGCTGGACCAACGTGAACATCGTGATGAATCATCGCAACTTGGACAGCGAGACCGGC 1020
 Db |||||
 QY 1937 GGCTGGACCAATGTAATATTGTCACTGAATATATCCGTAACTGATAGTGAACAGGG 1996
 QY 1021 GCCATGGTGGCGCTGCTGGAGGAGCGGA 1049
 Db |||||
 QY 1997 GCAATGGTGGCGCTGCTGGAAGATGGCGA 2025

RESULT 7

ABT08148
 ID ABT08148 standard; DNA; 4960 BP.

XX AC ABT08148;

XX 28-NOV-2002 (first entry)

XX Recombinase domain-containing fusion protein-related vector 4.

XX Fusion protein; recombinase domain; signal peptide domain; gene function;
 KW nuclear import; recombinase recognition sequence; transgenic organism;
 KW C31-Int recombination system; site-specific integration; gene therapy;
 KW vector; ds.

XX Unidentified.

XX WO200238613-A2.

XX 16-MAY-2002.

XX 09-NOV-2001; 2001WO-EF12975.

XX 10-NOV-2000; 2000EP-0124629.

XX 17-APR-2001; 2001EP-0109543.

XX 13-AUG-2001; 2001US-311876P.

XX (ARTE-) ARTEMIS PHARM GMBH.

XX Kuehn R, Felder S, Schwenk F, Kueter-luks B, Faust N;

XX WPI; 2002-519298/55.

XX Novel fusion protein useful for recombining DNA molecules in eukaryotic
 PT cells has recombinase protein which is linked to signal peptide domain
 PT which directs nuclear import of fusion protein in eukaryotic cells -

XX Example 1; Page 55-56; 150pp; English.

XX

CC The invention comprises the amino acid and coding sequences of fusion
 CC proteins that contain a recombinase domain and a signal peptide domain
 CC which directs nuclear import of the fusion protein in eukaryotic cells.
 CC The fusion proteins of the invention are useful for recombining the DNA
 CC molecules of cells or organisms containing recombinase recognition
 CC sequences for the recombinase domain of the fusion proteins. The fusion
 CC proteins of the invention are useful for studying gene function at
 CC various developmental stages and for the creation of transgenic
 CC organisms. The C31-Int recombination system of the invention can be used
 CC for the site-specific integration of foreign DNA into the genome of
 CC mammalian cells (e.g. for gene therapy). The present DNA sequence
 CC represents a vector that was used in the invention.

XX

SQ Sequence 4960 BP; 1225 A; 1213 C; 1296 G; 1226 T; 0 other;

Query Match 60.9%; Score 639.4; DB 24; Length 4960;

Best Local Similarity 75.6%; Pred. No. 2.3e-85;

Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 1 ATGCCCAAGAAGAGGAGGTGAGCAACCTGCTGACCGTGCACAGAACCTGCCCGCC 60
 Db |||||
 QY 977 ATGCCCAAGAAGAGGAGGTGCTCAATTTACTGACCGTACACCAAAATTTGCTGCA 1036
 Db |||||
 QY 61 CTGCCCGTGGACGCCACACGACGAGGTGGCAAGAACTGATGACATGTTCCCGAC 120
 Db |||||
 QY 1037 TTACCGGTGATGCAACGAGTGTGAGGTTCGCAAGAACCTGATGACATGTTCAAGGAT 1096
 Db |||||
 QY 121 CGCAGCGCTTCAGCGAGCACACCTGGGAAGTGTCTGAGCGTGTGCCGACGCTGGGC 180
 Db |||||
 QY 1097 CGCAGCGCTTTCTGAGCATACCTGGAANAATGTTCTGCTGTTGCCGCTGCTGGCG 1156
 Db |||||
 QY 181 GCCTGTGCAAGCTGAACACCGCAAGTGTGTTCCCGCGAGCCCGAGACGTCGCCGAC 240
 Db |||||
 QY 1157 GCATGTGCAAGTTGAATAACCGGAATGTTTCCCGAGAACCTGAAGATGTTCCGAT 1216
 Db |||||
 QY 241 TACTGCTGTACTGACGCCCGCGCTGGCGGTGGAAGACCATCCAGCAGCACTGGGC 300
 Db |||||
 QY 1217 TATCTTCTATATCTTCAGCGCGCGTCTGGCAGTAAATAATATCCAGCAACATTTGGC 1276
 Db |||||
 QY 301 CAGCTGAACATGTGTCACCGCGCAGCGGCTGCCCGCCCGCAGCGACGACGACGCGCTG 360
 Db |||||
 QY 1277 CAGTAAACATGCTTCATCGTCCGGCTGCCACGACCAAGTGACAGCAATGCTGT 1336
 Db |||||
 QY 361 AGCTGTGTGATCGCCGCAATCCGCAAGAGAACCTGCAACCGCGCAGCGCGCAAGCAG 420
 Db |||||
 QY 1337 TCACTGTTTATCGCGGATCCGAAAGAAACGTTGATGTCGGGTGAACGTCGAAACAG 1396
 Db |||||
 QY 421 GCTCTGCTTGGAGCGACCGACTTCGACCGAGTGGCAGCGCTGATGAGAACACGCGAC 480
 Db |||||
 QY 1397 GCTCTAGCGTTCGACGCACTGATTTCCGACCAGGTTGCTTCACTCATGAAAAATAGCGAT 1456
 Db |||||
 QY 481 CGCTGCCAGGACATCCGCAACCTGGCTTCTTGGGATCGCTTACACACCCCTGCTGCGC 540
 Db |||||
 QY 1457 CGTCCAGATATACGTAATCTGGCAATTTCTGGGATTTGCTTATACACCCCTGTTACGT 1516
 Db |||||
 QY 541 ATGCCCGAGATCGCCGCAATCCGCGTGAAGGACATCAGCCGACCGACGCGCGCCCATG 600
 Db |||||
 QY 1517 ATAGCGAAATGCCAGGATCAGGTTAAAGATATCTACGTACTGACGGTGGGAAATG 1576
 Db |||||
 QY 601 CTGATCCACATCGCGCGACCAAGACCTGTGTGAGCACCGCGCGGTGGAGAGGCCCTG 660
 Db |||||
 QY 1577 TTAATCCATATTGGCAGAACGAAACCGTGTGTAGCACCGCAGGTGTAGAGAGGCACCT 1636
 Db |||||
 QY 661 AGCCTGGGCTGACCAAGCTGTGGGCGCTCGATCAGGTGAGCGGCTGCGCCGACGAC 720
 Db |||||
 QY 1637 AGCCTGGGGTAACATAACTGCTGAGCGATGGAATTCGTTCTCTGTGTGATGATGAT 1696
 Db |||||
 QY 721 CCCAACAACTACTGTTTCTGCGCGTGGCAGAGACGGGTGTGCCGCCCGCCCGACCC 780
 Db |||||
 QY 1697 CGAATAACTACTGTTTTCGCGGTGAGAAAAAATGTTGTGCCCGCCATCTGCCACC 1756
 Db |||||
 QY 781 AGCCAGCTGAGCACCGCGGCCCTGGAGGCGCATCTTGAGGCGCACCCACCGCCTGATCTAC 840
 Db |||||

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Db 1757 AGCCAGCTATCAACTCGCGCCCTGGAAGGGATTTTGAAGCAACTCATCGATTGATTAC 1816
Qy 841 GGCGCCAGGACGACAGCGGCAGCGCTACCTGCGCTGGAGCGGCACAGCGCCGCGTG 900
Db 1817 GCGCTAAGGATGATCTGCTGTCAGAGATACCTGCGCTGCTGGACACAGTGCCTGTC 1876
Qy 901 GCGCGCCGCCGACATCGCGCCGCGCGCGCTGAGCATCCCGAGATCATCGAGCGCGC 960
Db 1877 GGAGCCGCGGAGATATGCGCGCGCTGAGTTTCAATACCGGAGATCATCAAGCTGGT 1936
Qy 961 GGCTGGACCAACGTGAACATCGTGATGAACACTACATCCGCAACCTGGACGAGACCGGC 1020
Db 1937 GCGTGGACCAATGTAATATTTGTATGAACATATATCCGTACCTGGATAGTGAAACAGG 1996
Qy 1021 GCCATGTGCGCTCTGGAGACGGCA 1049
Db 1997 GCAATGGTGGCGCTGCTGGAAGTGGCGA 2025

RESULT 8
AAD04928
ID AAD04928 standard; DNA; 5365 BP.
AC
XX AAD04928;
XX
DT 17-JUL-2001 (first entry)
DE Retroviral vector pBABE-pgkCre used as gene trap in embryonic stem cells.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; retroviral vector;
KW pBABE-pgkCre; cre recombinase; phosphoglycerate kinase; PGK promoter; ds.
XX
OS Chimeric - Moloney murine leukemia virus.
OS Chimeric - Mus sp.
OS Chimeric - Bacteriophage P1.
OS Chimeric - Rhesus macaque polyoma virus.
XX
PH Key Location/Qualifiers
FT LTR 8..480
FT /*tag= a
FT /note= "5', partial MMLV U3, MMLV R and MMLV U5"
FT /partial
FT 8..335
FT /*tag= b
FT /note= "5', partial MMLV U3"
FT /partial
FT 336..402
FT /*tag= c
FT /rpt_type= DIRECT
FT /note= "5', MMLV R direct repeat"
FT 403..480
FT /*tag= d
FT /note= "5', MMLV U5"
FT 481..1374
FT /*tag= e
FT /note= "MMLV primer binding site and extended
FT packaging signal"
FT 1417..1921
FT /*tag= f
FT /note= "Mouse phosphoglycerate kinase (PGK) promoter"
FT 1972..3024
FT /*tag= g
FT /product= "Bacteriophage P1 Cre recombinase protein with
FT a simian virus 40 large T-antigen N-terminal nuclear
FT localisation signal"
FT 3088..3168
FT /*tag= h
FT /note= "Promoter/enhancer deleted MMLV U3"
FT 3187..3332
FT /*tag= i
FT /note= "3', MMLV R and MMLV U5"
FT

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FT repeat_unit /partial
FT 3187..3253
FT /*tag= j
FT /rpt_type= DIRECT
FT /note= "3', MMLV R direct repeat"
FT 3254..3332
FT /*tag= k
FT /note= "3', MMLV U5"
XX
FN WO200129208-A1.
XX
XX 26-APR-2001.
XX
XX 16-OCT-2000; 2000WO-BF10162.
XX
XX 16-OCT-1999; 99EP-0120592.
XX
XX 27-OCT-1999; 99US-0162016.
XX
XX (ARTE-) ARTEMIS PHARM GMBH.
XX (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
XX Kuehn R, Von Melchner H, Altschmied J;
XX
XX MPI; 2001-308486/32.
XX
XX New gene trapping construct capable of causing conditional mutations in
XX genes, comprises functional DNA segment inserted in sense or antisense
XX direction relative to gene to be trapped -
XX
XX Example 1; Page 55-57; 78pp; English.
XX
XX The present invention relates to a conditional gene trapping construct
XX capable of causing conditional mutations in genes. The gene trapping
XX construct comprises two functional DNA segments, each being flanked by
XX two recombinase recognition sequences (RRSs) specific to site specific
XX recombinase which is capable of unidirectional inversion of double
XX standard DNA segment. One of the DNA segment (disruption cassette) is
XX inserted in antisense orientation relative to the transcriptional
XX orientation of the gene to be trapped. The other DNA segment (selection
XX cassette) is inserted in sense direction relative to the transcriptional
XX orientation of the gene to be trapped. The cell comprising the gene
XX trapping construct is useful for the identification and/or isolation of
XX genes. The transgenic organism comprising the gene trapping construct is
XX useful to study gene function at various developmental stages. The gene
XX trapping construct is useful for mutationally inactivating all cellular
XX genes. The present sequence is retroviral vector pBABE-pgkCre which is
XX used as a gene trap in embryonic stem (ES) cells. The vector
XX pBABE-pgkCre is constructed by inserting Bacteriophage P1 cre recombinase
XX coding region with a simian virus 40 large T-antigen N-terminal nuclear
XX localisation signal and mouse phosphoglycerate kinase (PGK) promoter into
XX Moloney murine leukemia virus based vector pBABEpuro.
XX
XX Sequence 5365 BP; 1208 A; 1448 C; 1402 G; 1307 T; 0 other;
XX
Query Match 60.9%; Score 639.4; DB 22; Length 5365;
Best Local Similarity 75.6%; Pred. No. 2.3e-85;
Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
Qy 1 ATGCCCAAGAAGAAGAGGAGGTGAGCAACCTGCTGACCGTGACCCAGAACCTGCCCGCC 60
Db 1972 ATGCCCAAGAAGAAGAGGAGGTGCTCAATTTACTGACCGTACACCAAAATTTGCTGCA 2031
Qy 61 CTGCCCGTGGAGCCACCGAGCGAGGTGCGCAAGACCTGATGGACATGTTTCGCGAC 120
Db 2032 TTACCGGTGATGCAACGAGTGATGAGGTTGCGAAGAACCTGATGGACATGTTTCAAGGAT 2091
Qy 121 CGCCAGGCGCTTCAGCGAGCACACCTGGAGAGTCTGCTGAGCGTGTGCGGAGCTGGCGC 180
Db 2092 CGCCAGGCGCTTTCTTGAGCATACCTGGAAATGCTTCTGCTCGGTTTTCGCGGTGGCGG 2151
Qy 181 GCCTGTGCAAGCTGAACCAACCGCAAGTGGTTCCCGCGAGCGAGCGACCTGCGCGAC 240
Db 2152 GCATGTGTGAAGTTGATTAACCGGAAATGTTTCCCGGAGAACCTGAAGATGTTTCGCGAT 2211

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Db 1239 GCCGAAATTCAGGATCAGGGTTAAAGATATCTCACGTACTGACGGTGGGAGATGTTA 1298
QY 604 ATCCACATCGCCGCCACCAACACCTCGTGTGAGCAGCCGCCGCTGGAGAGCCCTGAGC 663
Db 1299 ATCCATATTTGGCAGAAAGAAACACCTCGTTAGCAGCCGAGGTGTAGAGAGGCACCTTAGC 1358
QY 664 CTGGCGGTGACCAAGCTGGTGGAGCGCTGGATCAGCGCTGAGCGGTGGCGGACGACCCC 723
Db 1359 CTGGGGGTAACTAAACTGGTTCGAGCGATGGATTTCCGTTCTCTGTGTAGCTGATGATCCG 1418
QY 724 AACAACTACTGTTTCTGCCGCGTGCAGCAAGAACGCGCTGGCGGCCGCCAGCCACCAGC 783
Db 1419 AATAACTACTGTTTTCGCCGGTTCAGAAATAATGGTGTGCGCGCCATCTGCCACCAGC 1478
QY 784 CAGCTGAGCACCAGCGGCTGGAGGCGATCTTCAGGCGACCCACCGCTGATCTAGCGC 843
Db 1479 CAGCTTCACTACGCGCCCTGGAGGGATTTTGAAGCAACTCATCGATTGATTTAGCGC 1538
QY 844 GCCAAGGACACAGCGGCCAGCGCTACTCGTGCCTGGAGCGGCCACAGCCCGCGTGGGC 903
Db 1539 GCTAAGATGACTCTGTGAGAGATACCTGGCCCTGGTCTGGACACAGTGCCCGTTCGGA 1598
QY 904 GCCGCCCGGACATGGCCCGCGCGGTGAGCATCCCGAGATCATCGAGCGCGCGGC 963
Db 1599 GCGCGCGAGATATGCCCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGC 1658
QY 964 TGGACCAACGTGAACATCGTGAATCACTATCCGGAACCTGGACAGCAGACCGCGGCC 1023
Db 1659 TGGACCAATGTAATATTTGTATGAACATATATCCGTAACCTGGATAGTGAACAGGGGCA 1718
QY 1024 ATGTCGCGCTGCTGGAGGCGGCA 1049
Db 1719 ATGGTGCCTGCTGGAGATGGCGA 1744
```

RESULT 11

```
AAH26331
ID AAH26331 standard; DNA; 5261 BP.
```

```
AC AAH26331;
```

```
XX 02-OCT-2001 (first entry)
```

```
XX Recombinant adenovirus delta-E1 Cre-LoxP Ad.
```

```
XX Adenovirus; delta-E1 Cre-LoxP Ad; adeno-associated virus; vector;
KW gene therapy; ds.
```

```
XX Chimeric - Mastadenovirus.
```

```
OS Chimeric - Human cytomegalovirus.
```

```
OS Chimeric - Rhesus macaque polyoma virus.
```

```
XX Key Location/Qualifiers
```

```
FT promoter 551..1186
```

```
FT /tag= a
```

```
FT /note= "CMV promoter"
```

```
FT polyA_site 2251..2476
```

```
FT /tag= b
```

```
FT /note= "SV40 polyA site"
```

```
FT misc_recomb 2476..2520
```

```
FT /tag= c
```

```
FT /function= "loxP site"
```

```
XX W0200155361-A2.
```

```
PN XX
```

```
XX 02-AUG-2001.
```

```
XX 26-JAN-2001; 2001WO-US02709.
```

```
XX 26-JAN-2000; 2000US-0178536.
```

```
XX (CHIR ) CHIRON CORP.
```

```
XX PA
```

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XX
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```
PI Hardy SP;
```

```
XX WPI; 2001-483239/52.
```

```
XX
```

```
PT Producing recombinant adeno-associated virus (rAAV) vector, by stably
PT infecting eukaryotic host cell with rAAV vectors, helper adenovirus or
PT herpes virus, recombinant adenovirus or herpes vectors -
```

```
XX Disclosure; Page 60-62; 63pp; English.
```

```
XX The present sequence is that of recombinant adenovirus delta-E1
CC Cre-loxP Ad, in which the E1 gene of the wild-type adenovirus is
CC substituted by plasmid DNA comprising a cytomegalovirus (CMV)
CC promoter inserted immediately downstream of the CMV promoter
CC followed by a sequence from SV40 that specifies polyadenylation in
CC mRNA, and a loxP site. The recombinant adenovirus is used as an
CC induction system in methods of the invention. Thus, methods
CC and compositions are provided for producing recombinant adeno-
CC associated virus (rAAV) vector particles by: (a) introducing into
CC a host cell (i) AAV packaging plasmid pflxAAV (see AAH26332), (ii)
CC a recombinant viral vector encoding plasmid, and (iii) a plasmid
CC encoding herpesvirus, cytomegalovirus or adenoviral functions, or
CC a herpesvirus, cytomegalovirus or adenovirus itself, to produce
CC flox AAV particles and rAAV particles; and (b) introducing into a
CC second host cell (i) the rAAV particles or (a), (ii) a vector
CC that directs expression of Cre, and (ii) a vector which directs
CC expression of herpes virus, cytomegalovirus or adenovirus helper
CC functions, such that rAAV vector particles are produced. The
CC vectors are useful for in vivo or in vitro gene therapy and also
CC for in vitro recombinant protein production.
```

```
XX Sequence 5261 BP; 1309 A; 1238 C; 1329 G; 1385 T; 0 other;
```

```
Query Match 60.0%; Score 630; DB 22; Length 5261;
```

```
Best Local Similarity 75.1%; Pred. No. 5.4e-84;
```

```
Matches 786; Conservative 0; Mismatches 260; Indels 0; Gaps 0;
```

```
QY 4 CCCAAGAAGAGGAGGTGAGCAACCTGCTGACCGTGCACAGACCTGACCGCGCTG 63
```

```
Db 1201 CCAAGAAGAAGAGGAGGTTCGAATTTACTGACCGTACACCAAAATTTGCCGTGATTA 1260
```

```
QY 64 CCGTGTGAGCCACACGACGAGGTGCGCAGAACCTGATGACATGTTCCCGACCGC 133
```

```
Db 1261 CCGGTGATGCAACGAGTGATGAGTTTCGCAAGAACCTGATGACATGTTTCAGGGATCGC 1320
```

```
QY 124 CAGCGCTTCAGCGAGCACACCTCGAAAGATGCTCTGAGCGTGTGCCGAGCTGGCGCGC 183
```

```
Db 1321 CAGCGCTTTCTGAGCATACCTGGAAATGCTTCTGTCGTTTCCGGTCTGGGGCGCA 1380
```

```
QY 184 TGGTGAAGCTGAACCAACCGCAAGTGGTTCGCCGCGAGCCGAGGACGTTGCCGACTAC 243
```

```
Db 1381 TGGTGAAGTTGAATTAACCGGAAATGGTTTCCCGCAGAACCTGAGATGTTCCGATTA 1440
```

```
QY 244 CTGCTGTACTCGAGCGCCGCGCTGGCGGTGAAGACCATCCAGCAGACCTGGGGCCAG 303
```

```
Db 1441 CTTCTATATCTTCAGGCGCGCGTCTGGCAGTAAAAAATATCCAGCAACATTTGGGGCCAG 1500
```

```
QY 304 CTGAACATGTGCACCGCGCAGCGGCTGCGCCGCCGCCAGCAGACGACCGCTGAGC 363
```

```
Db 1501 CTAAACATGCTTCATGTCGTTCCGGCTGCCAGGACCAAGTGACAGCAATGCTGTTTCA 1560
```

```
QY 364 CTGGTGAATGCGCGCATCCGCAAGGAGAACGTGGACCGCGCGAGCGCCCAAGCAGCGCC 423
```

```
Db 1561 CTGGTTATGCGCGGATCCGAAAGAGAAACGTTGATGCGCGTGAACTGTCGCAAAACAGGCT 1620
```

```
QY 424 CTGGCCTTCGAGCGCACCGACTTCGACGAGGTGCGCAGCCTGATGAGAGAACGCGCCAGC 483
```

```
Db 1621 CTAGCGTTCGAACGCACTGATTCGACCGAGGTTCGTTCACTCATGTGAAAAATAGCGATCGC 1680
```

```
QY 484 TGCAGGACATCCGCAACCTGGCTTCCTGGGCGATCGCCTACAAACCTGCTGCCCATC 543
```

```
Db 1681 TGCCAGGATATAGTAACTCTGGCATTTCTGGGATTTGCTTTATAACACCTGTTACGTATA 1740
```



```
QY 544 GCCGAGATCGCCGATCCGGTGAAGACATCAGCCGACCGACCGCGCGCGCGATCTG 603
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1741 GCCGAATTCGAGGATCAGGGTTAAAGATATCTCAGTACTGACGGTGGGAAATGTTA 1800
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 604 ATCCACATCGCCGACCAAGACCTCGTGAGACACCGCCGCGTGGAGAGGCCCTGAGC 663
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1801 ATCCATATTGGCAGAACGAAACCGCTGGTTAGACCCGAGGTGTAGAGAGGCATTTAGC 1860
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 664 CTGGCGTGACCAAGCTGGTGGAGCGCTGTGATCAGCGCGTGGCCGACGACCCC 723
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1861 CTGGGGGTAACTAAACTGGTCGAGCGATGGATTTCCGCTCTGTGGTGTAGCTGATCCG 1920
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 724 AACCACTACCTGTTCTCGCGGTGCGCAAGACCGCGTGGCCGCCCGACGCGACAGC 783
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1921 AATAACTACCTGTTTTCGCGGGTCAGAAAAAATGGTTGCGCGCCATCTGCACACGC 1980
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 784 CAGCTGAGCACCGCGGCTGGAGGGCATCTTCGAGGCCACCCACCGCTGTATACGGC 843
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1981 CAGTATCACTCGCGCCCTGGAAGGATTTTGAAGCACTCATCGATTGATTACGGC 2040
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 844 GCCAAGACGACGCGCCAGCGCTACTCTGCGCTGGAGCGGCCACAGCCCGCGTGGC 903
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2041 GCTAAGATGACTCTGGTTCAGAGATACCTGGCCTGGTCTGACACAGTGGCCGTCGGA 2100
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 904 GCCGCCCGACATGSCCGCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGGC 963
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2101 GCCCGCGAGATATGGCCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGTGGTGGC 2160
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 964 TGGACCAACGTGAACATCGTGATGAACCTATCATCGCAACCTGGACAGCGAGACCGCGGC 1023
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2161 TGGACCAATGTAATATTGTTCATGAACCTATATCCGTAACCTGGATGTGAACAGGGGCA 2220
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1024 ATGTGCGCTGTGGAGGCGGCA 1049
Db 2221 ATGTGCGCTGTGGAGATGGCGA 2246
```

RESULT 12

AAC62541
ID AAC62541 standard; DNA; 1172 BP.

AC AAC62541;

DT 07-FEB-2001 (first entry)

XX Cre wild-type coding sequence.

XX Cre variant recognition site; lox site; recombinase;

XX variant recombination site; hybrid crop production; seedless crop;

XX phage packaging; cloning; ds.

XX Unidentified.

XX WO200060091-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09154.

XX 06-APR-1999; 99US-0127977.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX Sauer BL, Rufer AW;

XX WPI; 2000-665010/64.

XX Identifying variant recombinases mediating recombination at variant
PT sites (vrs) by contacting a mutant recombinase, a first and second vrs
PT having a reporter gene, and a second nucleic acid having 2 vrs and a
PT reporter gene -

PS Example 1; Page 98-101; 144pp; English.

XX

CC The present invention relates to the identification of recombinase
CC variants which have an altered specificity. They are tested using
CC constructs containing variant recognition sites, which are not recognised
CC by non-mutant recombinase but undergo recombination in the presence of a
CC variant enzyme. Variant recombinases are useful in the production of a
CC genetically modified crop plants, particularly seedless varieties, and in
CC phage packaging, which has uses in cloning.

XX SQ Sequence 1172 BP; 299 A; 263 C; 323 G; 287 T; 0 other;

Query Match 59.2%; Score 621.8; DB 21; Length 1172;

Best Local Similarity 74.5%; Pred. No. 1e-82;

Matches 782; Conservative 0; Mismatches 267; Indels 0; Gaps 0;

QY 1 ATCCCCAAGAAGAGGAGGTGAGCAACCTCTGACCGTGACAGAACCTGCGCGCC 60

Db 35 ATCCTCTAGACTGAGTGTGAATGTCCAATTTACTGACCGTACACCAAAATTTGCTGCA 94

QY 61 CTGCCCCGTGAACCCACCGACGAGGTGCGCAAGAACTGATGACATGTTCCCGGAC 120

Db 95 TTACCGGTGATGCAACGAGTGTGATGAGTTTCGCAAGAACTGATGACATGTTTCAGGAT 154

QY 121 CGCCAGGCTTCAGCGAGCACACCTGGAAGATGCTGCTGAGCGTGTGCCGACTGGGC 180

Db 155 CGCCAGCGTTCCTGAGCATACCTGGAATAATGCTTCTGTCGTTTTCGCGGTCTGGCGG 214

QY 181 GCCTGCTGAAGCTGAACACCGCAAGTGTGTTCCCGCGGAGCCCGAGGACGTGCGGAC 240

Db 215 GCATGCTGAAGTTGAATTAACCGAATGTTTCCCGCAGAACCTGAAGATGTTCCGAT 274

QY 241 TACTGCTGTACTCTGAGGCGCGCGCTGGCGTGAAGACATTCAGAGCACCTGCGGC 300

Db 275 TATCTTCTATCTTCAGGCGCGGTCTGGCAGTAAATAATATCCAGCAACATTTGGGC 334

QY 301 CAGCTGAACATGCTGACCGCGCGCGCTGCCCGCGCCGAGCAGACGACGCGGTG 360

Db 335 CAGCTAAACATGCTTCATGTCGGTCCGGCTCCACGACCAAGTACAGCAATGCTGTT 394

QY 361 AGCTGTGTGATGCGCGCATCCCGAAGAGAACTGGAAGCGCGCGAGCGCGCAAGCAG 420

Db 395 TCACTGTTATGCGCGGATCCGAAAGAAAAGTTGATGTCGCGTGAACGTGCANAACAG 454

QY 421 GCCTGCGCTTCAGCGCACCGACCTTCGACCGAGTGGCGAGCCTGATGAGAGACAGGAC 480

Db 455 GCTCTAGCGTTCGAACGCACTGATTTTCGACCAAGTTCGTTCACTCATGGAATAAGCAT 514

QY 481 CGCTGCGAGACATCCGCAACCTGCGCTTCCTCGGCATCGCTTACAAACCCCTGCTGCGC 540

Db 515 CGCTGCGAGATATAGTAACTGCGCATTTCTGGGATTTCTTAAACCCCTGTTACGT 574

QY 541 ATCGCCGAGATCGCCGATCCCGGTGAAGGACATCAGCCGCAACCGACGCGCGCGCATG 600

Db 575 ATAGCGAAATTCGAGGATCAGGGTTAAAGATATCTCAGTACTACGCTGGGGAATG 634

QY 601 CTGATCCATATCGCGCGCACCAAGACCTGCTGTGAGCACCGCGCGGTGGAGAGGCCCTG 660

Db 635 TTAAATCCATATTGGCAGAAACGCTGGTTAGCACCGCGAGGTGTAGAGAGGACATT 694

QY 661 AGCTGCGGTGACCAAGCTGGTGGAGCGCTGATCAGCGTGGCGCGTGGCGCGGAC 720

Db 695 AGCTGGGGTAACCTAACTGGTCGAGCGATGATTTCCGTCTCTGTGTAGCTGATGAT 754

QY 721 CCCAACAACCTACCTGTTCTGCGCGTGCAGAAAGCGGTGTGCGCCGCCCGCCGCGCAC 780

Db 755 CCGAATAACTACCTGTTTTCGCGGTGAGAAAATGTTGTCGCGCGCATCTGCCACC 814

QY 781 AGCAGCTGAGACCCGCGCGCTGGAGGATCTTCGAGGCCACCCACCGCTGTATCTAC 840

Db 815 AGCAGCTATCAACTCGCGCGCTGGAAAGGATTTTGAAGCAACTCATCGATTGATTAC 874

QY 841 GCGCCCAAGGACGACAGCGCGCGCTACCTTGGCTGGAGCGCGCACAGCGCGCGGTG 900

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 875 GGCCTAAGGATGACTCTGCTCAGAGATACCTGSCCTGGTCTGACACAGTGCCTCGTGC 934
 QY 901 GCGCCGCGCGGACATGGCCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGC 960
 Db 935 GGAGCCGCGGAGATATGGCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT 994
 QY 961 GGCTGGACCAACGTGAACATCGTATCAACTACATCCGCAACCTGGACAGCGAGACGGC 1020
 Db 995 GGCTGGACCAATGTAATATTGTTCATGAATATATCCGTAACTATGATAGTGAACACAGG 1054
 QY 1021 GCCATGCTGGCCCTGCTGGAGGACGGCA 1049
 Db 1055 GCAATGCTGCCCTGCTGGAGATGGCA 1083

RESULT 13

ABN97179

ID ABN97179 standard; DNA; 1553 BP.

XX AC ABN97179;

XX 13-AUG-2002 (first entry)

DT Gene #3677 used to diagnose liver cancer.

XX Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX Homo sapiens.

XX W020229103-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US30589.

XX 02-OCT-2000; 2000US-237054P.

XX (GENE-) GENE LOGIC INC.

XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX WFI; 2002-426119/45.

XX Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample

XX Claim 1; SEQ ID NO 3677; 298pp; English.

XX The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

Query Match

Best Local Similarity 58.9%; Score 618.4; DB 24; Length 1553;

Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAAGGTGAGCAACCTGCTGACCGTGCACAGAAACCTGCCCGCCTGCCCGTGGACG 73
 Db 477 AGTGTTAAATGTCCAAATTTACTGACCGTATACCAAAATTTGCTGCAATTACCGGTGCATG 536
 QY 74 CCACCAAGCAGCAGGCTGCGCAAGAACCTGATGACATGTTCCGCGACCGCCAGGCGCTTCA 133
 Db 537 CAACGAGTGATGAGGTTCCGAGAACCTGATGACATGTTTCAGGATTCGCGAGCGTTTT 596
 QY 134 GCGAGCACACCTGGAAAGATGCTGCTGAGCGTGTGCCGCGAGCTGGCGCGCTGGTCAAGC 193
 Db 597 CTGAGCATACCTGGAAAAATGCTTCTGTCGTTTGCCGCTCGTGGCGGATGGTGCAGT 656
 QY 194 TGAACAAACCGCAAGTGGTTCCCGCGCAGCCCGAGGACGTGCGCGCATCTACCTGCTTACC 253
 Db 657 TGAATAAACCGGAAATGGTTTCCCGCAGAAACCTGAAGATGTTGCGGATTATCTTCTATATC 716
 QY 254 TGCAGGCGCGCGCTGGCGCTGGAAGACCATCAGCAGACACCTGGCGCGAGCTGGAACATGC 313
 Db 717 TTCAGCGCGCGCTCTGGCAGTAAAACTATCAGCAACATTTGGGCCAGCTAAACATGC 776
 QY 314 TGCACCGCGCAGCGCGCTGCCCGCCCGCAGCAGCAACCGCGTAGCGCTGGTATGC 373
 Db 777 TTCATGCTCGTCCGGCTGCCAGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGC 836
 QY 374 GCGCATTCGCAAGGAGAAAGTGGAGCCGCGGAGCGCGCCGAAGCAGCGCCTGGCCTTCG 433
 Db 837 GCGCGATCCGAAAGAAAAACGTTGATGCCGCTGAACGTGCAGCAACAGAGGCTCTAGCGTTCG 896
 QY 434 AGCGCACCGACTTCGACACAGGTGCGCAGCGCTGATGGAGAACAGCGCGCTGCCAGACA 493
 Db 897 AACGCACTGATTTGCGACCAAGTTCGTTTCACTCATGGAAAAATAGCGATTCGCTGCCAGATA 956
 QY 494 TCCGCAACCTGGCCTTCTGGGCGATCGCCTACAACACCTGCTGCCCATCGCGAGATCG 553
 Db 957 TAGTAACTGCGCATTTCTGGGGATTGCTTATAACACCTCTTACGTATAGCGAAATTG 1016
 QY 554 CCGCATTCGCGGTGAAGGACATCAGCCGCAACGAGCGCGCGCATCTGCTGATCCACATCG 613
 Db 1017 CCAGGATCAGGGTTAAAGATATCTACGTACTGACGCTGGGAGATGTTAAATCCATATTG 1076
 QY 614 GCGCAGCAAGACCTCGTGGAGCACCGCGCGGTGGAGAAAGCCCTGAGCCTGGGCGTGA 673
 Db 1077 GCAGAAACGAAAAACGCTGGTTAGCACCGCAGGTGTAGAGAAAGGCACCTTAGCCTGGGGTAA 1136
 QY 674 CCAAGCTGTGGAGCGCTCGATCAGCGTGAGCGCGCTGCGCAGACACCCCAACACTACC 733
 Db 1137 CTAAACTGTGCGAGCGATGGAATTCGCTCTCTGCTGATGATGATCCGATAACTACC 1196
 QY 734 TGTTCTGCGCGTGCACAAAGACGGCGTGGCGCCCCCGCAGCGCCACCGCAGCTGAGCA 793
 Db 1197 TGTTTTCGCGGGTFCAGAAAAATGGTGTTCGCGCGCATCTGCCACAGCAGCTATCAA 1256
 QY 794 CCGCGCCCTGGAGGCGATCTTCGAGGCCACCCCGCTGATCTACGCGGCCCAAGGACG 853
 Db 1257 CTGCGCCCTGGAGGGGATTTTGAAGCAACTCATCGATTGATTACGCGCGCTAAGGATG 1316
 QY 854 ACAGCGCGCAGCGCTACCTGGCGCTGGAGCGGCCACAGCGCCCGCGCGCGCGCGCG 913
 Db 1317 ACTCTGTCAGAGATACCTGGCTGTGTGGACACAGTGCCTGTCGAGCGCGCGCGAG 1376
 QY 914 ACATGCGCGCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGCGCGCTGACCAACG 973
 Db 1377 ATATGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGCTGCTGGCAACATG 1436
 QY 974 TGAACATCGTATGAACTACATCCGCAACTGACAGCAGACCGCGCGCATGTGCGCC 1033
 Db 1437 TAAATATTGTCATGAATATATCCGTACCTGATAGTAGTGAACAGGCGCAATGGTGC 1496
 QY 1034 TGCTGGAGGACGCGCA 1049
 Db 1497 TGCTGGAGATGGCGA 1512

RESULT 14
 AAD35276
 ID AAD35276 standard; DNA; 1553 BP.
 XX
 AC AAD35276;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Bacteriophage P1 Cre recombinase DNA.
 XX
 KW Site-specific DNA recombinase; DR1; membrane translocation sequence; MTS;
 KW cell-permeable recombinase; nuclear localisation signal; NLS; excretion;
 KW trafficking; blood-brain barrier; gene; ds.
 XX
 OS Bacteriophage P1.
 XX
 PN W020020737-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US28209.
 XX
 PR 07-SEP-2000; 2000US-230690P.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Ruley HE, Jo D;
 XX
 DR WPI; 2002-362248/39.
 XX
 PT New isolated polypeptide comprising a cell-permeable site-specific DNA
 PT recombinase and membrane translocation sequence for stimulating
 PT site-specific DNA recombination in a cell -
 XX
 PS Example 1; Page 66-67; 70pp; English.
 XX
 CC The invention relates to a polypeptide comprising a site-specific
 CC DNA recombinase (DR1) and a membrane translocation sequence (MTS),
 CC and nucleic acids that encode such cell-permeable recombinases. The
 CC sequences of the invention are useful for stimulating site-specific
 CC DNA recombination in a cell and for determining the efficiency of
 CC protein transduction into a population of cells. The polypeptide of
 CC the invention is further useful for detecting whether site-specific
 CC DNA recombination has occurred within a cell and for identifying a
 CC compound that modulates nuclear metabolism in a cell. It is used for
 CC identifying a peptide that behaves as a membrane translocation or
 CC nuclear localisation signal (NLS) and is also useful for identifying
 CC a compound preferably an amino acid sequence that modulates the
 CC delivery of a polypeptide to a cell or the activity of a polypeptide
 CC in a cell, where the compound modulates trafficking, uptake, excretion
 CC or other activity of a specific therapeutic protein, by enhancing
 CC protein delivery across the blood-brain barrier. The present sequence
 CC is Bacteriophage P1 Cre recombinase DNA.
 XX
 SQ Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

Query Match 58.9%; Score 618.4; DB 24; Length 1553;
 Best Local Similarity 74.8%; Pred. No. 3.1e-82;
 Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACCTGCTGACCGTGACACAGAACCTGCCCGCCCTGCCGTGAGC 73
 DB 477 AGTGTAAATGTCCAAATTTACTGACCGTACACCAAAATTTGCGCTGCAATTACCGGTGATG 536
 QY 74 CCACGAGCGAGGTGCGAAGAACCTGATGGACATGTTCCGGGACCGCGAGCCCTTCA 133
 DB 537 CAACGATGATGAGTTGCGAGAGACCTGATGGACATGTTGAGGATCGCGAGCGTTT 596
 QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGGTGTGCCGAGCTGGCGCGCTGTGTGCAAGC 193
 DB 597 CTGAGCATACCTGGAATAATGCTTCTGTCCGTTTTCGCGGTGTGGGCGCATGTGTGAAGT 656

QY 194 TGAACAAACCGCAAGTGGTTCCCGCGGAGCCCGAGAGCGTGGCGACTACCTGCTGTACC 253
 DB 657 TGAATAACCGGAATGGTTTCCCGCAGAACCTTGAAGATGTTCCCGATTATCTTCTATATC 716
 QY 254 TGCAGGCCCGCGCGCTGGCGGTGAAGACCATCAGCAGCACCTGGCCAGCTGAACATGC 313
 DB 717 TTCAGGCGCGCGTCTGGCAGTAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGC 776
 QY 314 TGCACGCGCGCAGCGCTTGCCTCCCGCCAGCGACAGCAACCGCTGAGCCTGGTGAATC 373
 DB 777 TTCACTCGTCCGTCGCGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGC 836
 QY 374 GCGCATCCGCAAGAGAGACGTGGACGCGCGGAGCGCGCCCAAGCAGGCGCTGGCCTTCG 433
 DB 837 GCGGATCCGAAAGAAAACGTTGATGCGCGTGAACGTGCAAAACAGGCTCTAGCGTTTCG 896
 QY 434 AGCGACCGACTTTCGACCAAGTGCAGCGCTGATGGAGAACAGCACCGCTGCCAGGACA 493
 DB 897 AACGCACTGATTTCCGACCAAGTTCGTTCACTCATGGAAATAGCGATCGTCCAGGATA 956
 QY 494 TCGCAACCTGGCCTTCTGGGATGCGCTACAACACCTGTGTGGCATCGCGAGATCG 553
 DB 957 TACGTAATCTGGCAATTTCTGGGATGCTTATAACACCTGTTACGTATAGCGAAATTC 1016
 QY 554 CCGCATCCGCTGAGGACATCAGCGCACCGACCGCGCGCGCATGCTGATCCACATCG 613
 DB 1017 CCAGGATCAGGTTAAAGATATCTCACGTACTGACGCTGGGAGATGTTAATCCATATTC 1076
 QY 614 GCGCACCAAGACCTCTGGTGAGCACCGCGCGGTGGAGAAAGCCCTGAGCCTGGGCGTGA 673
 DB 1077 GCAGAACGAAACGCTGTTAGCACCGCAGGTGTAGAGAAAGCACTTAGCCTGGGGTTAA 1136
 QY 674 CCAAGCTGTGAGCGCTCGATCAGGTGAGCGCGGTGGCGCAGACGCCCAACAACTACC 733
 DB 1137 CTAAACTGTGCGAGCGATGGATTTCCGTCTCTGCTGTAGCTGATGATCCGAATAACTACC 1196
 QY 734 TGTCTGCGCGTGGCGAAGAACGGTGGCGCGCCCGCCAGCGCCACCGAGCTGAGCA 793
 DB 1197 TGTTTTGCGGGTTCAGAAAAATGGTGTGCGCGCCATCTGCCACCGCCAGCTATCAA 1256
 QY 794 CCGCGCCCTGAGAGGCATCTTCGAGGCCACCCACCGCTGATCTACGGCGCCAGGACG 853
 DB 1257 CTCGCGCTTGGNAGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGATG 1316
 QY 854 ACAGCGCGCAGCGCTACCTGCGCTGAGCGGCGCACAGCCCGCGTGGCGCGCCCGCG 913
 DB 1317 ACTCTGTCAGAGATACCTTGGCGCTGCTCTGGACACAGTCCCGCTGTCCGAGCGCGCAG 1376
 QY 914 ACATGCGCGCGCGCGTGAGCATCCCGAGATCATGCGCGCGCGCTGACCAACG 973
 DB 1377 ATATGCGCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGTGTGACCAATG 1436
 QY 974 TGAACATCGTGAATACATCCGCAACTCGGACAGCGAGACCGCGCGCATGTGTGCGCC 1033
 DB 1437 TAAATATTGTCATGAATATATCCGTAACTGGATAGTGAACAGGGGCAATGTTGTCGCC 1496
 QY 1034 TGCTGAGGACGCGCA 1049
 DB 1497 TGCTGAGATGCGCA 1512

RESULT 15
 ABK10252
 ID ABK10252 standard; DNA; 1553 BP.
 XX
 AC ABK10252;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Bacteriophage P1 Cre site specific recombinase gene.
 XX
 KW Transgenic plant; site-specific recombinase; transgene excision;
 KW Cre; Cre/Lox; DNA excising gene cassette; ds.

XX Bacteriophage P1.
 OS WO200210415-A2.
 PN 07-FEB-2002.
 XX 27-JUL-2001; 2001WO-US23794.
 XX 28-JUL-2000; 2000US-221318P.
 PR (UYCO-) UNIV CONNECTICUT.
 XX Li Y, O'donnell CP, Duan H, Wu YH, Mcavoy R;
 XX WPI; 2002-217124/27.
 DR
 XX
 XX Creating a transiently transgenic plant for producing non-transgenic
 PT food products, comprises introducing a gene cassette having
 PT multifunctional transgenic DNA sequences which excise themselves from
 PT the genome -
 XX
 PS Example 1; Page 51; 58pp; English.
 XX
 CC This invention relates to a novel method for creating a transiently
 CC transgenic plant. The method comprises introducing a gene cassette
 CC containing transgenic gene sequences conferring a desirable phenotypic
 CC trait, a recombinase-type protein, sequences cleavable by a recombinase
 CC protein and a promoter to a plant. The plant is then exposed to a
 CC stimulus that activates the promoter and directs expression of the
 CC recombinase protein which excises the heterologous DNA from the plant
 CC genome. This method is useful for creating a transiently transgenic
 CC plant where a heterologous transgene temporarily conveys a desired
 CC phenotypic trait to the plant. Complete or nearly complete removal of
 CC the heterologous DNA reduces the possibility of uncontrolled propagation
 CC of the transgenic species and permits crops produced from the transgenic
 CC plants to be co-mingled with non-transgenic crops for marketing
 CC purposes. The method is useful for producing non-transgenic food
 CC products from transgenic plants. The excision of the transgene occurs
 CC only after the transgenic functions are either no longer needed, or the
 CC continued presence of transgenes could cause concern. If transgenes are
 CC excised from the host genome in response to a stimulus several days
 CC prior to harvesting or marketing, potential negative effects of the
 CC transgenes are reduced or eliminated. The progeny of the plants are also
 CC essentially free of the transgene sequences. The method helps to reduce
 CC potential health implications of transgenic food, to eliminate
 CC undesirable spread of transgenes to the environment because pollen and
 CC seeds produced from transgenic plants are non-transgenic, and to
 CC protect proprietary rights inherent in the transgenic technology.
 CC The present sequence represents the bacteriophage P1 Cre site specific
 CC recombinase gene sequence, this sequence recognises the LoxP sequence.
 CC The Cre/Lox site specific recombinase system may be used in the method
 CC of the invention to excise heterologous DNA from a plant.
 XX
 SQ Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

Query Match 58.9%; Score 618.4; DB 24; Length 1553;
 Best Local Similarity 74.8%; Pred. No. 3.1e-82;
 Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACTGCTGACCGTGACACGAGACCTGCCCGCCTGCCCGTGACG 73
 Db 477 AGTGTAAATGTCGCAATTTACTGACCGTACACCAAAATTTGCCCTGCATTACCGGTCGATG 536
 QY 74 CCACGACGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACCGCCAGCCCTTCA 133
 Db 537 CAACGATGATGAGTTTCGCAAGAACCTGATGGACATGTTTACGGGATCGCCAGCGGTTT 596
 QY 134 GCGAGCACACTGGAAGATGCTGCTGAGCGGTGTCGCGCAGCTGGCGCGCCTGTGTGCAAGC 193
 Db 597 CTGAGCATACCTGGAAAATGCTTCTGTCGCTTTCGCGGTGCTGCGCGCATGGTCAAGT 656
 QY 194 TGAACACCGCAAGTGTGTTCCCGCCGAGCCGAGGACGTTGCGCGACTACCTGCTGTACC 253

Db 657 TGAATAACCGGAATGTTTCCCGCAGAACCTGAAGATGTTCCGGATTATCTTCTATATC 716
 QY 254 TGCAGGCCCGCGCCTGGCCGTGAAGACCATTCAGCAGACACCTGGGGCAGCTGAACATGC 313
 Db 717 TTCAGGCGCGCGTCTGGCAGTAAAACTATTCAGCAACATTTGGGCCAGCTAAACATGC 776
 QY 314 TGCACCGCCGACAGCGCTGCCCGCCCGCCAGCGACAGCAACGCGCTGAGCTGTGTATGC 373
 Db 777 TTCATCGTGGTCCGGCTGCCACGACCAAGTAGACAGCAATGCTGTGTTTCACTGGTTATGC 836
 QY 374 GCGCATCCGCAAGGAGAACGTGAGCGCGCGAGCGCGCAAGCAGCGCCCTGGCCTTCG 433
 Db 837 GCGGATCCGAAAGAAACGTTGATGCCGTTGAACGTGCAAAACAGGCTCTAGCGTTCG 896
 QY 434 AGCGCACCGACTTTCGACACAGGTGCGCAGCTGTATGGAGAACAGCAGCCGCTGCCAGACA 493
 Db 897 AACGCATGATTTGACACAGGTTTCGTTCACTCATGGAANAATAGGATCGCTGCCAGATA 956
 QY 494 TCCGCAACCTGGCCTTCCTGGGGCATCGCCTAACACACCTCTGTGCGCATCGCCGAGATCG 553
 Db 957 TACGTAATCTGGCATTTCTGGGATTTCTTATAACACCTCTGTACGTATAGCCGAAATTG 1016
 QY 554 CCCGCATCCGCGTGAAGGACATCAGCGGACCGACCGCGCCGCTGCTGATCCACATCG 613
 Db 1017 CCAGGATCAGGGTTAAGATATCTCAGTACTCAGCGTGGGAGAAATGTTAATCCATATTG 1076
 QY 614 GCGCCACCAAGACCTCTGTTGAGCACCGCGCGCTGGAGAGAGCCCTGAGCCTGGGCGTGA 673
 Db 1077 GCAGAACGAAACGCTGGTTAGCACCGCAGGTCTAGAGAGGACACTTAGCCTGGGGTAA 1136
 QY 674 CCAAGCTGTGGAGCGCTGGATCAGCGTGAAGCGCGTGGCCGACGACCCCAACAACCTACC 733
 Db 1137 CTAACCTGTGTCGAGCATGATTTCCGCTCTCTGCTGTAGTGTATGATCCGATAACTACC 1196
 QY 734 TGTCTTCCGCGCTGCCAGAACGCGGTGCGCGCCGCCCGCCAGCGCACCGACCTGAGCA 793
 Db 1197 TGTTTTGCGGGTCAGAAAAAATGGTGTTCGCCGCGCCATCTGCCACCCAGCCGCTATCAA 1256
 QY 794 CCCGGGCGCTGGAGGGCATCTTCAGGCCACCCACCGCCTGATCTAGCGGCGCAAGGACG 853
 Db 1257 CTCGCGCCCTGGAAGGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGATG 1316
 QY 854 ACAGCGCCAGCGCTACCTGGCTGGAGCGGCCACAGCGCCGCGCTGGCGCGCCGCGCG 913
 Db 1317 ACTCTGTCAGAGATACCTGGCCTGCTGGAACAGTGCCTGTCGGAGCGCGCGAG 1376
 QY 914 ACATGGCCGCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGGTGACCAACG 973
 Db 1377 ATATGGCCGCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATG 1436
 QY 974 TGAACATCGTGAATAACTACATCCGCAACTGAGACAGCGAGACCGCGCGCATGCTGGCGCC 1033
 Db 1437 TAAATATTGTCATGAATACTATATCCGTAACTCTGATAGTGAACAGGGGCAATGCTGCGCC 1496
 QY 1034 TGCTGAGGACGCGCA 1049
 Db 1497 TGCTGAGAGATGGCGA 1512

Search completed: December 16, 2003, 01:47:41
 Job time : 370 secs

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QM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 01:32:08 ; Search time 86 Seconds

(without alignments)
5388.980 Million cell updates/sec

Title: US-09-662-128A-1

Perfect score: 1050

Sequence: 1 atgccaagaagaaggaa.....gcctgtgaggagcgcgac 1050

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755	71.9	2346	3	US-09-193-503B-5
2	755	71.9	2346	4	US-09-415-839-5
3	754.4	71.8	1032	3	US-09-193-503B-2
4	754.4	71.8	1032	4	US-09-415-839-2
5	630	60.0	5261	4	US-09-770-315-7
6	617.4	58.8	1740	2	US-08-864-224-10
7	617.4	58.8	2346	3	US-09-193-503B-4
8	617.4	58.8	2346	4	US-09-415-839-7
9	617.4	58.8	2346	3	US-09-193-503B-8
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11	617.4	58.8	2346	4	US-09-415-839-7
12	617.4	58.8	2346	4	US-09-415-839-8
13	616.6	58.7	4491	4	US-08-837-863-23
14	241.2	23.0	699	2	US-08-735-609-11
15	241.2	23.0	699	2	US-08-735-609-11
16	241.2	23.0	699	3	US-09-315-372-11
17	241.2	23.0	699	3	US-09-244-752-11
18	241.2	23.0	699	3	US-09-245-497-11
19	241.2	23.0	699	4	US-09-562-919-11
20	88.6	8.4	2163	4	US-09-252-991A-5310
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22	88.6	8.4	4158	4	US-09-252-991A-5348
23	88.6	8.4	4953	4	US-09-252-991A-5227
24	88.2	8.4	3624	1	US-07-951-715A-6
25	88.2	8.4	3624	2	US-08-459-448A-6
26	88.2	8.4	3624	3	US-08-459-595A-6
27	88.2	8.4	3624	3	US-08-459-504B-6

28 88.2 8.4 3624 3 US-08-459-444-6 Sequence 6, Appli
29 88.2 8.4 3624 3 US-09-053-549-7 Sequence 7, Appli
30 88.2 8.4 3624 4 US-09-547-422-6 Sequence 6, Appli
31 87.6 8.3 3222 4 US-09-543-084A-29 Sequence 29, Appli
32 86.6 8.2 3468 1 US-07-951-715A-2 Sequence 2, Appli
33 86.6 8.2 3468 2 US-08-459-448A-2 Sequence 2, Appli
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35 86.6 8.2 3468 3 US-08-459-504B-2 Sequence 2, Appli
36 86.6 8.2 3468 3 US-08-459-444-2 Sequence 2, Appli
37 86.6 8.2 3468 4 US-09-053-549-3 Sequence 2, Appli
38 86.6 8.2 3468 4 US-09-547-422-2 Sequence 7, Appli
39 86 8.2 4039 4 US-09-205-448-7 Sequence 26, Appli
40 86 8.2 4050 4 US-09-543-084A-26 Sequence 2, Appli
41 86 8.2 4093 4 US-09-543-084A-28 Sequence 4, Appli
42 85.6 8.2 975 3 US-09-365-150-4 Sequence 28, Appli
43 85.4 8.1 4767 4 US-09-231-899-76 Sequence 76, Appli
44 85.2 8.1 1965 3 US-09-178-252-26 Sequence 26, Appli
45 84.4 8.0 2929 4 US-09-543-084A-31 Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-09-193-503B-5

; Sequence 5, Application US/09193503B

; Patent No. 6262341

; GENERAL INFORMATION:

; APPLICANT: Baszczynski, Christopher L.

; APPLICANT: Lyznik, Leszek A.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Guan, Xueni

; APPLICANT: Rao, Guru

; APPLICANT: Tagliani, Laura A.

; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into

; FILE REFERENCE: 5718-66 (amended listing)

; CURRENT APPLICATION NUMBER: US/09193,503B

; CURRENT FILING DATE: 1998-11-17

; PRIOR APPLICATION NUMBER: 60/099,435

; PRIOR FILING DATE: 1998-09-08

; PRIOR APPLICATION NUMBER: 60/056,627

; PRIOR FILING DATE: 1997-11-18

; PRIOR APPLICATION NUMBER: 60/065,613

; PRIOR FILING DATE: 1997-11-18

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 2346

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: sequence

; OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage p1 and

; OTHER INFORMATION: FLP from Saccharomyces, both maize preferred

; OTHER INFORMATION: Codons

; NAME/KEY: CDS

; LOCATION: (1)..(2346)

US-09-193-503B-5

Query Match

Best Local Similarity 71.9%; Score 755; DB 3; Length 2346;

Matches 857; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Qy 23 TGAGCAACCTGCTGACCGTGCACGAACTGCGCCGCTGCGCGTGGAGCCGACCG 82

Db 2 TGTCACCTGCTGCTGACCGTTCACGAACTTCCGAGTGGAGCGGACGTCG 61

Qy 83 ACGAGTGCACAGAACTGATGACATGTCGCGACCGCCAGGCTTCAGCGAGCACA 142

Db 62 ATGAAGTCAGGAGAACTCATGACATGTTCCGCGACAGCAAGCTTCAGCGAGCACA 121

Qy 143 CCTGGAAGATGCTGCTGAGCGTGTGCGGAGCTGGGCGCGCTGGTGTGACGACCAACC 202

542	Db	CGGTGAAGGACATTAGCGCACCGACGGCGCAGGATGCTATTCCATTGGCAGGACCA	601
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602	Db	AGACGCTGTTTCACCGCAGCGCTCGAAGAAGGCCCTCAGCCTCGGAGTGACCAAGCTCG	661
683	Qy	TGGAGCGCTGGAATCAGCGTGAGCGCGGTGGCCGACGACCCCAACAATCACTGTTCTTGCC	742
662	Db	TCGAACGCTGGATCTCCGTGTCGCGCGTCCGGGACGACCCAAAACAATCACTCTCTCTGCC	721
743	Qy	CGCTGCGCAAGAAGCGGTGGCGCCGCCCCAGCGCCACACGACCTGAGCACCGCGGCC	802
722	Db	CGCTCCGCAAGAAGCGGGTGCTGCCCCCTAGCGCCACGAGCAACTCAGCACGAGGCGCT	781
803	Qy	TGGAGGGCATCTTCGAGGCCCACCAACCGCCTGATCTACGGCGCCAAAGACGACAGCGGCC	862
782	Db	TGGAAGGTATTTTCGAGGCCACCAACCGCCTGATCTACGGCGCGAAGATGACAGCGGTC	841
863	Qy	AGCGCTACTCGCTGGAGCGGCGACAGCGCCCGGTGGGGCGCCGCCCGGACATGCGCC	922
842	Db	AACGCTACTCGCATGGTCCGGGCACTCCGCGCGCTGGAGCTGCTAGGACATGCGCC	901
923	Qy	GGCGCGGTGAGCATCCCGAGATCATGACGGCGCGCGGTGAGCCCAACGCTGACATCG	982
902	Db	GGCGCGGTGTTTCCATCCCCGAAATCATGAGCGGGGTGGATGGACCAACGCTGAACATTG	961
983	Qy	TCATGAATACATCCGAACCTGGACAGCGAGACCGCGCCATGGTGCCTGCTGGAGG	1042
962	Db	TCATGAATCAATTCGCAACCTTGACAGCGAGACGGGCGCAATGGTTCGCTCTCGAAG	1021
1043	Qy	ACGGCGA	1049
1022	Db	ATGGCGA	1028

RESULT 3

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US-09-193-503B-2
; Sequence 2, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence encoding Cre protein from Bacteriophage
; OTHER INFORMATION: P1, maize preferred codons (moCRE)
US-09-193-503B-2

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Query Match	71.8%	Score 754.4;	DB 3;	Length 1032;
Best Local Similarity	83.4%	Pred. No. 3.5e-120;		
Matches 857; Conservative	0;	Mismatches 171;	Indels 0;	Gaps 0;

QY	23	TGAGCAACCTGCTGACCGTGCACAGAAACCTGCCCGCCCTGCCGTGGAGCGCCACACGCG	82
DB	2	TGTCCAACCTGCTCAACGGTTTCACAGAAACCTCCGGCTCTCCAGTGGAGCGCAGCTCCG	61
QY	83	ACGAGGTGCGCAAGAACTCATGATGGAATGTTCCGCGACACCGCAGGCTTCAGCGAGCACA	142
DB	62	ATGAAGTCAGGAGAACTCATGGAATGTTCCGCGACAGCGAAGCGTTCAGCGAGCACA	121
QY	143	CTTGGAAAGATGCTGCTGAGCGTGTGCGCGAGCTTGGCGCGCTGGTGAAGCTGAAACAAC	202
DB	122	CCTGGAAAGATGCTGCTCTCGCTCTGCCCGCTTCCTGGGCTGATGCTGAAGCTGAAACAAC	181
QY	203	GCAAGTGTGTTCCCGCGCGAGCCGAGAGACGTGCGCGACTACCTGCTGTACTCTCCAGCGCC	262
DB	182	GGAAGTGTGTTCCCGCTGAGCCGAGACGTGAGGATTAACCTTGTGTAACCTGCAAGCTC	241
QY	263	CGCGCTTGGCGTGAAGAACCATCCAGCAGACCTTGGGCCAGCTGAACATGCTGCACCGCC	322
DB	242	CGCGGCTGGCAGTGAAGAACCATCCAGCAACACTTGGACAACATGAATGCTTTCACAGGC	301
QY	323	GCAGCGGCTTCCCGCGCCAGCGACAGCAAGCAAGCGCGTGTGATCGGCGGCAATCC	382
DB	302	GCTCCGCGCTCCCGCGCCAGCGACTCGAAGCGCGTGAGCCTCGTCATGCGCGCATCA	361
QY	383	GCAAGAGAACTGTGAGACCGCGGAGCGCGCCCAAGCAGAGGCCCTTGGCTTCGAGCGCACCG	442
DB	362	GGAAGAAACGTCGATGCCGCGGAAGGCAAGCAGCGCCCTGCGCTTCGAGAGGACCG	421
QY	443	ACTTTCGACAGGTGCGCAGCGCTGATGAGAAACAGCGACCGCTGCGCAGGACATCCGCAACC	502
DB	422	ATTTCGACCAAGTCCGAGCGCTGATGAGAAACAGCGACAGGTGCGCAGGACATTAGGAACC	481
QY	503	TGGCCTTCTGGGCATCGCTTAAACACCTGTGCGCATCGCGGAGATCGCCGCGATCC	562
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DB	542	CGCTGAAGGACATTAGCCGACCGACCGCGCGCAGGATGCTTATCCATTTGGCAGGACCA	601
QY	623	AGACCTTGTTGAGCACCGCGCGGTGAGAAAGGCGCTGAGCCTGGGCGTGAACAAAGTCG	682
DB	602	AGACGCTCTGTTTCCACCGCAGGGGTGAAAAGGCGCTTCAGCCTCGGAGTGACCAAGCTCG	661
QY	683	TGAGCGCTCGATCAGCGTGAGCGGCTGCGCGACGACCCCAACACTACTGTTCTGTC	742
DB	662	TCGAACTGGAATCTCGTGTCTGGGCTGCGGACGACCCAACTACTCTTCTGTC	721
QY	743	CGGTGCGCAAGACGGCGTGGCGCCGCCACAGCGCACACCGCAGCTGAGCACCGGCGCC	802
DB	722	CGGTCCGCAAGAACGGGCTGGCTGCCCTTAGCGCACACAGCCAACCTCAGCACAGGCGCT	781
QY	803	TGAGGGCACTTCTGAGGCCACCCACCGCTGATCTACGCGGCGCAGGACGACAGCGGCC	862
DB	782	TGGAAGGTATTTTCAGGGCCACCCACCGCTGATCTACGCGCGGAAGGATGACAGCGGTC	841
QY	863	AGCGCTACCTGGCTGAGCGGCGCACAGCGCCCGCGTGGCGCGCGCGACATGGCGCC	922
DB	842	AACGCTACCTCGCATGTCTCGGGCACTCCGCGCGCTTGGAGCTGTAGGGAATGGGCC	901
QY	923	CGCGCGCGTGAAGATCCCGAGATCATGTCAGCGCGCGGCTGGACAACGTCGAAACATCG	982
DB	902	CGCGCGGTGTTTCCATCCCCGAAATCATGTCAGCGCGGTGGATGGAGAACGTCGAACTTG	961
QY	983	TGATGAACATCATCCGCAACTGACAGCGAGACCGCGCGCATGCTGGCGCTCTCGAGG	1042
DB	962	TCATGAACATCATTCGCAACTTGAACGCGAGACGGCGCAATGGTTTCGCTCTCTGGAAG	1021
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DB	1022	ATGGTGAC	1029


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Db 1261 CCGGTGATGCAACAGTGTAGTTCGCAAGAACCTGATGGACATGTTTCAGGATCGC 1320
Qy 124 CAGCCCTTACGAGACACCTGGAAGATGCTGTGAGCGTGTGCGCAGACTGGGCGGC 183
Db 1321 CAGCGGTTTCTGAGCATACCTGGAATACTGCTGTCCGTTTCCCGGTGTCGGCGGCA 1380
Qy 184 TGGTGAAGCTGACACACCGCAAGTGTTCCTCCCGCAGCCGAGGACGTCGCGACTAC 243
Db 1381 TGGTGAAGTTGAATAACCGGAATGTTTCCCGCAGAACCTGAAGATGTCGCGATTAT 1440
Qy 244 CTGCTGTACCTGACGCGCGCGCTGCGCTGAGACCAATCCAGCAGCACCTGGGCGAG 303
Db 1441 CTTCTATATCTTACGGCGCGGCTGCGCAGTAAATACTATCCAGCAACTTTGGGCGAG 1500
Qy 304 CTGAACATGTCACCCCGCAGCGGCTGTGCCCCCGCCGACGACGACGCGGTGAGC 363
Db 1501 CTAACATGTTTCATCGTCGCTCGGCTGCGCAGCAGCAAGTACAGCAATGCTGTTCA 1560
Qy 364 CTGCTGATGCGCGCATCCGACAGGAGAACTGACGCGCGGAGCGCGGCAAGCGGC 423
Db 1561 CTGCTGATGCGGCGGATCCGAAAGAAACGTTGATCCCGTGAACCTGCAAAACAGGT 1620
Qy 424 CTGCGCTTCAGCGCACCGCTTCCACAGGTGCGCAGCTGTAGGAGAACAGCGACCGC 483
Db 1621 CTAGCGTTCGACCGCACTGATTCGACAGCGTTCGTTCACTCATGGAATAGCGATCGC 1680
Qy 484 TGCAGACATTCGCAACCTGGCTTCTTGGGATCGCCTTACACACCCCTGTGCGCATC 543
Db 1681 TGCAGGATATACGTAATCTGGCATTTCTGGGGATTGCTTATAACACCTGTTACGTATA 1740
Qy 544 GCGAGATCCCGCATCCGGTGAAGACATCAGCCGACCGACCGCGCGCGCGCATCTG 603
Db 1741 GCGGAATGCCAGGTCAGGGTTAAAGATATCTCAGTACTGACGTGGGAGAAATGTTA 1800
Qy 604 ATCCACATCGCGCGCACAGACCTCGTGAGCACCGCGCGGTGGAGAGGCGCTGAGC 663
Db 1801 ATCCATATTCGAGAACGAAACGCTGTTAGCACCGAGGTGTAGAGAGGCACTTAGC 1860
Qy 664 CTGGGCTGACCAAGCTGTGGAGCGCTGTGATCAGCGTGTAGCGCGTGGCGGACGCC 723
Db 1861 CTGGGGTAACTAACTGGTCGAGCGATGGATTTCCGTCTCTGTGTGTAGCTGATCGC 1920
Qy 724 AACNACTACCTGTTCTCGCGTCCGCAAGAACGCGTGGCGCGCCCGAGCGGCACGAGC 783
Db 1921 AATAACTACCTGTTTTCGCGGTGAGAAAAAATGTTGTCGCGCGCATCTGCGCACGAGC 1980
Qy 784 CAGCTGAGCACCGCGCGCTGGAGGCGATCTTCAGGCGCACCCACCGCTGATCTACGGC 843
Db 1981 CAGTATCACTCGCGCTTGAAGGATTTTGAAGCACTCATCGATTGATTACGGC 2040
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Db 2041 GCTAAGGATGACTCTGTGTCAGAGATACCTGCGCTGTGTGACACAGTGGCCGTCGGA 2100
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Db 2101 GCGCGCGGATATGGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGC 2160
Qy 964 TGGACCAAGCTGAACATGATGAATACATTCGCAACCTTGGACAGCGAGACCGCGGC 1023
Db 2161 TGGACCAATGTAATATTTGTCATGACTATATCCGTAACCTTGGATAGTGAACAGGGGCA 2220
Qy 1024 ATGTTGCGCTGTGAGGAGCGGCA 1049
Db 2221 ATGTTGCGCTGTGAGGAGTGGCA 2246
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RESULT 6

US-08-864-224-10

; Sequence 10, Application US/08864224

; Patent No. 5851808

; GENERAL INFORMATION:

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; APPLICANT: Ellledge, Stephen J.
; APPLICANT: Liu, Qinghua
; TITLE OF INVENTION: Rapid Subcloning Using Site-Specific
; TITLE OF INVENTION: Recombination
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,224
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: BCM-02681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1737
; US-08-864-224-10
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Query Match 58.8%; Score 617.4; DB 2; Length 1740;
Best Local Similarity 75.1%; Pred. No. 6.1e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 23 TGAGCAACTGTGACCGTGCACAGAACTGCCGCCCTGCCCGTGGAGCGCCACCGAGC 82
Db 710 TGGCCAATTACTGACCGTACACCAAAATTTGCTTCATTACCGTTCGATGCAACGAGTG 769
Qy 83 ACAGGTGCGCAGAAGCTGATGACATGTTCCGACCGCCAGGCTTCAGCGAGCACA 142
Db 770 ATGAGGTTGCAAGAACCTGATGGACATGTTTCAGGGATCCGACGGCTTTTCTGAGCATA 829
Qy 143 CCTGGAAGATGCTGCTGAGCGTGTGCGCAGCTGGGCGCGCTGCTGCAAGCTGAACAAC 202
Db 830 CCTGGAAGATGCTTCTGTCGTTTGGCGGCGCATGTTGCAAGTTGAATTAAC 889
Qy 203 GCAAGTGGTTCCTCCCGCGAGCCCGAGGACGTCGCGCACTACCTGCTGTACCTCAGGCCC 262
Db 890 GGAATGGTTTCCCGCAGAACCTGAAGATGTTCCGATTATCTTCTATATCTTTCAGGCGC 949
Qy 263 GCGCGCTGGCGGTGAGACCATCCAGGACCATCTGGGCGAGCTGAACATGCTGACCGCC 322
Db 950 GCGGTCTGGCAGTAAAACTATCCAGCAACTTTGGGCCAGCTTAAACATGCTTTCATCGTC 1009
Qy 323 GCAGCGCTGCCCCCGCCAGGACGACGAAACCGCTGAGCGCTGGTGTGCGCGCATCC 382
Db 1010 GGTCCGCGTCCCGACGACCAAGTGACAGCAATGCTGTTTCTACCTGGTTATGCGGCGGATCC 1069
Qy 383 GCAAGGAGAACGTGGAGCGCGCGAGCGCGCCAGAGGCGCTTGGGCTTCGAGCGCACCG 442
Db 1070 GAAAGAAACGTTGATGCGGTGAACGTGCAAAACAGGCTCTAGCGTTTGAACGCACTG 1129
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443	QY	ACTTCGACGAGTGGCGAGCCTGATGAGAA	CGAGACGCTGCGCAGGACATCCGCAACC	502	
1130	Db	ATTTTCGACCAAGGTTCTGTTCACTCATG	GGAAAATAGCGATCGCTGCCAGGATATACGTAATC	1189	
503	QY	TGCGCCTTCCTGGGCATCGCTACAA	CACCCCTGTGCGCATCGGCCGAGATCGCCCGCATCC	562	
1190	Db	TGCGATTTCTGGGGATGTCCTTATA	CACCCTGTTAGTATAGCCGAAATGCCAGGATCA	1249	
563	QY	GCGTGAAGGACATCAGCCGCA	CCGACGCGCGCCCGCATGCTGATCCACATCGGCCGCAACA	622	
1250	Db	GGGTAAAGATATCTCA	CGTACTGACGGTGGGAGAATGTTAATCCATATTGGCAGAACGA	1309	
623	QY	AGACCTTGTTGACACCGCCGCGT	GGAGAGCCCTGTAGCCTGGGCGTGACCAAGCTGG	682	
1310	Db	AAACGCTGGTTAGCACCGCAGGT	TGAGAAGGCATTTAGCCTGGGGGTTAACTAATCTGG	1369	
683	QY	TGAGCGCTGGATCAGCGT	GAGGGCGCTGGCCGACGACCCCAACAACACTCTGTTCTGCC	742	
1370	Db	TCGAGCGATGGAITTCGTCT	CTGGTGTAGCTGATGATCGGAATACTACCTGTTTGGCC	1429	
743	QY	CGGTGCGCAAGAACGGCGT	TGGCGCCCCCAGCGCCACACAGCAGCTGAGCACCCGGGCC	802	
1430	Db	GGGTCAAGAAAAATGGTGT	TGCGCGCCATCTGCCACACGACGACTATCAACTCGCGCCC	1489	
803	QY	TGAGGGCATCTTCGAGCGCA	CCACCACCGCCTGATCTACGGCGCCCAAGACGACAGCGGCC	862	
1490	Db	TGGAAGGATTTTGAAGCA	ACTCATCGATTGATTACGGCGCTAAGATGACTCTGCTC	1549	
863	QY	AGCGTACCTGGCTGGAGCG	GGCCACAGCGCCCGCGTGGCGCGCCCGCGACATGGGCC	922	
1550	Db	AGAGATACCTGGCCTGGTCT	GGACACAGTGC	CCGTGTCGAGCGCGCGAGATATGGCCC	1609
923	QY	CGCGCGCGGTGAGCAT	CCCCGAGATCATCGAGCCGCGCGCTGACCAAGTGAACATCG	982	
1610	Db	CGCGTGAAGTTTCAATAC	CCGAGATCATGCAAGCTGTGGCTGGACCAATGTAATATTG	1669	
983	QY	TGATGAACATCATCCGCA	AACTCGACAGCGAGACCGCGCCCATGGTGGCGCTCTGTGAGG	1042	
1670	Db	TCATGAACATATATCCGT	AATCCGTGATAGTGAAACAGGGGCAATGGTGGCGCTCTGGAAG	1729	
1043	QY	ACGGCGA	1049		
1730	Db	ATGGCGA	1736		

RESULT 7

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US-09/193-503B-4
; Sequence 4, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-86 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence

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Db 902 GCCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
QY 983 TGATGAACATACCTCCGAACCTGGACAGCGAGACCGCGCATGTGGCTGCTGGAGG 1042
Db 962 TCATGAATATATCCGTAACTGGATAGTGAACACAGGGCAATGGTGGCTGCTGGAAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 8
US-09-193-503B-7
; Sequence 7, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding a Cre:FLP polypeptide, Cre from
; OTHER INFORMATION: Bacteriophage P1 and FLP from Saccharomyces

US-09-193-503B-7

Query Match 58.8%; Score 617.4; DB 3; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGACAGAACCTGCGCCGCTGCGGCGGAGCGCCACCGCG 82
Db 2 TGGCCAAATTACTGACCGTGACACCAAAATTGGCTGATTAACCGGTGATGCAACGAGTG 61
QY 83 ACGAGTGGCGAAGAACTGATGACATGTTCCGCGACCGCGCCCTCAGGAGGACA 142
Db 62 ATGAGGTTCGAAGAACTGATGACATGTTCCAGGATCGCGCGCTTTCTGAGCAT 121
QY 143 CCTGGAGATGCTGCTGAGCGTGGCGCGAGCTGGCGGCGCTGGTGAAGTGAACAAC 202
Db 122 CCTGGAAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
QY 203 GCAAGTGGTTCCTGCGGAGCGCGGAGCGAGCTGCGGAGCTGCTGCTGCTGCTGCTGCT 262
Db 182 GGAATGGTTCCTGCGGAGCGCGGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
QY 263 GCGGCTGGCGGTGAAGACCATCAGCAGCACTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCT 322
Db 242 GCGGCTGGCAGTAAAGTATATCCAGCAACATTTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCT 301
QY 323 GCACGCGCTGCG 382
Db 302 GGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGCGCGGATCC 361

QY 383 GCAAGGAGAACGTGGACCGCGCGGAGCGCGCCACGAGCGCCCTGGCTTTCGAGCGCACCG 442
Db 362 GAAAGAGAAACGTTGATCGCGTGAAACGTTGCAAAAACAGGCTTAGCGTTTCGAAACGCACTG 421
QY 443 ACTTCGACAGAGTGGCGACGCTGATGAGAGAACAGAGACCGCTGCCAGAGACATCCGCAAC 502
Db 422 ATTTTCGACAGAGTGGTTCACCTCCTGGAATAATGAGATCGCTGCCAGGATATACGTAATC 481
QY 503 TGGCCTTCTGGGCTATCGCTTACAACACCTCTGCGCATCGCCGAGATCGCCCGCATCC 562
Db 482 TGGCATTTCTGGGATTTCTTATAACACCTCTTACGTATACCGGAAATTCGAGGATCA 541
QY 563 GCGTGAAGACATGACCGCGACCGAGCGCGCGCATGCTGATCCACATCGCGCGCACCA 622
Db 542 GGGTTAAAGATATCTCACGTACTGACGGTGGGAGAAATGTTAATCATATATTCGAGAACGA 601
QY 623 AGACCTGCTGAGCACCGCGCGCTGGAGAGCGCTGAGCGCTGAGCGCTGGCGGTGACCAAGCTGG 682
Db 602 AAACGCTGTTAGCACCGCGAGGTGTAGAGAGGACCTTAGCTTGGGGTAACTAACTGG 661
QY 683 TGGAGCGCTGATCAGCGCTGAGCGCGTGGCGGAGCGACCGCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGCTCTCTGGTGTAGCTGATGATCCGAATAACTACCTGTTTGGC 721
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QY 803 TGGAGGCGATCTTCGAGGCGACCGCGCTGATCTACCGCGCGCGCGCGCGCGCGCGCGCG 862
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QY 863 AGCGCTTACCTGCGCTGGAGCGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 922
Db 842 AGAGATACCTGCGCTGGTCTGGACACAGTGCCCGTGTGGAGCGCGCGCGAGATATGGCC 901
QY 923 GCGCGCGCTGAGCATCCCGAGATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
Db 902 GCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
QY 983 TGATGAACATACCTCCGAACCTGGACAGCGAGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
Db 962 TCATGAACATATATCCGTAACTGGATAGTGAACACAGGGGCAATGGTGGCGCTGCTGGAAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 9
US-09-193-503B-8
; Sequence 8, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 8
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
; OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
; OTHER INFORMATION: from Bacteriophage P1
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-09-193-503B-8

Query Match      58.8%; Score 617.4; DB 3; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGCACAGAACCTGCCCGCCCTGCCCGTGCAGCGCCACACGCG 82
Db 1316 TGGCAATTTACTGACCGTACACCAAAATTTGCTGCATTAACCGTGCATGCAAGAGTG 1375

QY 83 ACAGAGTGCAGAAACCTGATGACATGTTCCGCGACCGCCAGGCGCTTCAGCGAGCACA 142
Db 1376 ATGAGGTTGCAAGAACCTGATGACATGTTTCAGGGATCGCAGCGCTTTTCTGAGCATA 1435

QY 143 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTGGCGCGCTGTGTGCAAGCTGAAACAAC 202
Db 1436 CTTGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1495

QY 203 GCAAGTGGTTCCTCCCGCGAGCCGAGGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 262
Db 1496 GGAATGGTTCCTCCCGCGAGCCGAGGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1555

QY 263 GCGGCTGGCGGTGAGAGACATCCAGCAGCACTGGGCGAGCTGAAACATGCTGCACGCC 322
Db 1556 GCGGCTGGCGGTGAGAGACATCCAGCAGCACTGGGCGAGCTGAAACATGCTGCTGCTGCT 1615

QY 323 GCAGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382
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QY 383 GCAAGGAGAGCTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 442
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QY 443 ACTTCGACAGGTGCGAGCGCTGTGAGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 502
Db 1736 ATTTCGACAGGTGCGAGCGCTGTGAGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1795

QY 503 TGGCCTTCCTGGGATTCGCTTACAAACCCCTGCTGCGCATCGCGAGATCGCGCGCATCC 562
Db 1796 TGGCATTTCTGGGGATTGCTTATAACACCCTGTTACGTTATAGCGGAAATGCCAGGATCA 1855

QY 563 GCGTGAAGGACATAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 622
Db 1856 GGGTTAAGATATCTCAGTACTGACGTTGGAGAGATGTTTATCCATATTGGCAGAACGA 1915

QY 623 AGACCTTGATGAGCACCAGCGCGGTGAGAGAGCGCGCTGAGCGCTGGCGGTGACCAAGTGG 682
Db 1916 AAACCTTGATGAGCACCAGCGGTGAGAGAGCGCGCTGAGCGCTGGCGGTGACCAAGTGG 1975

QY 683 TGGAGCGTGGATAGCGGTGAGCGCGGTGGCGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCG 742
Db 1976 TCGAGCGATGGAATTTCCGCTCTCTGCTGTAGCTGATGATCCGAAATAACTACCTGTTTTC 2035

QY 743 GCGTGGCAAGAACCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 802
Db 2036 GCGTGGCAAGAACCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2095

QY 803 TGGAGGGCATCTTCGAGGCGCACCCACCGCTGATCTACGGCGCCAGGACGACGCGGCC 862
Db 2096 TGGAGGGCATCTTCGAGGCGCACCCACCGCTGATCTACGGCGCCAGGACGACGCGGCC 2155
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QY 863 AGCGTACCTGGCTGGAGCGCGCCACAGCGCCCGTGGCGCGCGCGCGCGCGCATGGCCC 922
Db 2156 AGAGATACCTGGCTGGTCTGTGACACAGTGCCTGCTGCGAGCGCGCGCGAGATATGGCCC 2215

QY 923 GCGCGCGCGTGGAGCATCCCGGAGATCATGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
Db 2216 GCGCTGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 2275

QY 983 TGATGAACCTACATCCCAACCTGGAGCAGGAGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
Db 2276 TCATGAACCTATATCCGTAACCTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAAG 2335

QY 1043 ACGGCGA 1049
Db 2336 ATGGCGA 2342

RESULT 10
US-09-415-839-4
; Sequence 4, Application US/09415839
; Patent No. 6541231
; GENERAL INFORMATION:
; APPLICANT: Basczynski, Christopher L.
; APPLICANT: Lyszynski, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6541231 Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/415,839
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US/09/193,503
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence encoding a Cre, FLPm polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-09-415-839-4
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Query Match      58.8%; Score 617.4; DB 4; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGCACAGAACCTGCCCGCCCTGCCCGTGCAGCGCCACACGCG 82
Db 2 TGGCAATTTACTGACCGTACACCAAAATTTGCTGCATTAACCGTGCATGCAAGAGTG 61

QY 83 ACAGAGTGCAGAAACCTGATGACATGTTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 142
Db 62 ATGAGGTTGCAAGAACCTGATGACATGTTTCAGGGATCGCAGGCGCTTTTCTGAGCATA 121

QY 143 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
Db 122 CTTGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181

QY 203 GCAAGTGGTTCCTCCCGCGAGCCGAGGACGTCGCGCGACTACCTGCTGCTGCTGCTGCTGCTG 262
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182	DB	GGAAATGGTTTCCGCGAAGACCTGGAAGATGTTCCGGATTATCTTCTATATCTTTCAGGCGC	241
263	QY	CGCGCTGGCGGTGAAGACCATCCAGCAGACACTGGGCCAGCTGAAACATGCTGCACCGCC	322
242	DB	CGCGTCTGGCAGTAAAAAATATCCAGCAACATTTGGGCCAGCTAAACATGCTTTCATCGTC	301
323	QY	GCAGCGCTGCCCGCGCCGAGCAGACAGCAACCGGTGAGCCCTGCTGATGCGCGCGCATCC	382
302	DB	GGTCCGGCGTCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGCGCGGATCC	361
383	QY	GCAAGGAGAACGTTGGAGCCGCGGAGCGGCCCAAGCAGAGCCCTTGGCTTCGAGCGCACCG	442
362	DB	GAAAGAAACGTTGATGCCGGTGAAACGTGCAAAACAGGCTCTAGCGTTCCGACGCACTG	421
443	QY	ACTTCGACAGGTCCGAGCGCTGATGAGAAACAGGACCGCTGCAGGACATCCGCAACC	502
422	DB	ATTTTCGACCAAGTTTCTGTTCACTCATGAAAAATAGCGATCGCTGCCAGGATATACGTAATC	481
503	QY	TGGCCTCTTCGGGCATCGCTTACAAACCCCTGCTGGCGCATCGCGAGATCGCCCGCATCC	562
482	DB	TGGCATTTCTGGGATTTGCTTTTAAACCCCTGTTACGTATAGCGAAATTCAGGATCA	541
563	QY	GCGTGAAGGACATCAGCGCGCACCGACCGCGCGCGCATGCTGTATCCACATCGGCGGACCA	622
542	DB	GGGTTAAAGATATCTCAGTACTCACCGTGGAGAAATGTTTAATCCATATTTGGCAGAACGA	601
623	QY	AGACCTCTGTGAGCACCGCGCGCTGGAGAGGCCCTGAGCCTGGGGGTGACCAAGCTGG	682
602	DB	AAAACGCTGTGTAGCACCGCAGGTGTAGAGAGGCACTTAGCCTGGGGTTAACTAACTGG	661
683	QY	TGGAGCGCTGGATCAGCGCTGAGCGCGTGGCGCGACGACCCCAACAATCCTGTTCTGGCC	742
662	DB	TCGAGCGATGATTTCCGTCCTGCTGTAGCTGATGATCCGAATACTACCTGTTTTGCC	721
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803	QY	TGGAGGGCATCTTCGAGGCCACCCACCGCCTGATCTAGCGCGCCAGCAGCAGCGGCC	862
782	DB	TGGAAGGATTTTTGAAGCAACTCATCGATTGATTTTACGGCGCTTAAGAGATGACTCTGTC	841
863	QY	AGCGTACTCTGGCTGGAGCGGCCACAGCGCCCGCTGGCGCGCCCGCAGCATGSCCC	922
842	DB	AGAGATACCTGGCCTGGTCTGGACACAGTGCCTGTCGAGCGCGCGAGATATGGCCC	901
923	QY	GGCGCGGCTGAGCATCCCCAGAGATCATGAGCGCGGCGCTGGACCAACGTGACATCG	982
902	DB	CGCTTGGAGTTTCAATATCCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG	961
983	QY	TGATGAATACATCCGCAACCTGGACACGAGACCGCGCCCATGGTGGCGCTGCTGGAGG	1042
962	DB	TCATGAATATATCGTTAACTGGATAGTGAACAGGGCAATGGTGGCCTGCTGGAAG	1021
1043	QY	ACGGCGA	1049
1022	DB	ATGGCGA	1028

RESULT 11
 US-09-415-839-7
 ; Sequence 7, Application US/09415839
 ; Patent No. 6541231
 ; GENERAL INFORMATION:
 ; APPLICANT: Baszczyński, Christopher L.
 ; APPLICANT: Lyznik, Leszek A.
 ; APPLICANT: Gordon-Kamm, William J.
 ; APPLICANT: Guan, Xueni
 ; APPLICANT: Rao, Guru
 ; APPLICANT: Tagliani, Laura A.
 ; TITLE OF INVENTION: A No. 6541231a1 Method For The Integration Of Foreign DNA
 ; TITLE OF INVENTION: Into
 ; TITLE OF INVENTION: Eukaryotic Genomes

Db 662 TCGAGCGATGGATTTCCTGCTCTCTGGTGTAGCTGATCCGAATAACTACCTGTTTGGCC 721
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Db 782 TGGAAAGGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGGATGACTCTGGTC 841
Qy 863 AGCGCTACCTGGCTGGAGCGGCCACAGCGCCCGGGTGGCGCCCGCCGACATGGGCC 922
Db 842 AGAGATACCTGGCGCTGGTGTGACACAGTGGCGGTGTGGAGCGCGCGAGATATGGCC 901
Qy 923 GCGCGCGCTGAGCATCCCGGAGATCATCAGCGCGCGCGCTGTGACCAACGTTGAACATG 982
Db 902 GCGCTGGAGTTTCAATACCGGAGATCATCAAGCTGGTGGCTGGACCAATGTAATATTG 961
Qy 983 TGTGAACTACATCCCACTTGGACAGCGAGACCGCGCCATGGTGGCGCTGCTGGAGG 1042
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RESULT 12

US-09-415-839-8
; Sequence 8, Application US/09415839
; Patent No. 6541231
; GENERAL INFORMATION:
; APPLICANT: Baszynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6541231 Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09415,839
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US/09193,503
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 2346

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Sequence

OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from

OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre

OTHER INFORMATION: from Bacteriophage P1

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(2346)

US-09-415-839-8

Query Match 58.8%; Score 617.4; DB 4; Length 2346;

Best Local Similarity 75.1%; Pred. No. 6.2e-97;

Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

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RESULT 13

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Qy 83 ACGAGGTGCGCAAGAACTGATGACATGTTCCGGACCGCGAGCCCTTACGCGAGACA 142
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Qy 323 GCAGCGGCTGCCCCCGCCAGCGACAGCAACGCGGTGAGCTGTGTGATGCGCGCATCC 382
Db 1616 GGTCCGGCTGCGCAGCACCAAGTACAGCAATGCTGTTCACCTGGTATGCGGGAATCC 1675
Qy 383 GCAAGGAGAACGTGGACCGCCGCGAGCGCGCAAGAGCGGCGCTTTCAGAGCGACCG 442
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Qy 443 ACTTCGACGAGTGGCGAGCGCTGTGAGACACAGCGAGCGCGCTGCGCGGATCCGCAACC 502
Db 1736 ATTTCCAGCAGGTTTCGTTTCACTCATGGAATAATAGCGATCGCTGCGCAGGATATACGTAATC 1795
Qy 503 TGGCGCTTCTGGCGCATCGCTTACACACCTCTCGCGATCGCGAGATCGCGCGCATCC 562
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DB	369	ATGTTTCCCGCAGAACTCAAGATGTTCCGATTTATCTTATATCTTCAGCGCGGG	428	
QY	267	CTCGGCGTGAAGACATCCAGCAGCACCTGGCGCAGCTGACATGCTGCACCGCGCAG	326	
DB	429	TCTGGCAGTAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGCTTCATCTCGGTG	488	
QY	327	CGGCTGCCCGCCCGACGACGACGACGCGCTGAGCTGGTGTATCGCGCGCATCCGCAA	386	
DB	489	CGGCTGCGCAGCACCAGTGACAGCAATGCTGTTTCACTGGTTATCGCGCGGATCGGAA	548	
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DB	549	AGAAAACTGATCGCGGTGAAACGTGCAAAACAGGCTTAGCGTTCGAAACGCACTGATTT	608	
QY	447	CGACGAGTGGCAGCTGATGGAGACACGACGACCGCTGCCAGGACATCCGCAACTGGC	506	
DB	609	CGACGAGTTCGTTTCACTCATGGAAAAATAGCGATCGCTGCCAGGATATACGTAATCTGC	668	
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DB	729	TAAAGATATCTCAGTACTGACGTTGGGAAATGTTAATCCATTTGGCAGACGAAAC	788	
QY	627	CTGTGTAGACACCGCGCGCTGGAGAGGCGCTGAGCTGGCGGTGACCAAGCTGTGGA	686	
DB	789	GCTGTTAGCACCGCAGGTGTAGAGAGGCACTTAGCTTGGGGTAACTAACTGGTCTGA	848	
QY	687	GCGCTGATTCAGCGTGAAGCGCGTGGCGGACGCCCAACATCTACTGTTTTCGCGGT	746	

GenCore version 5.1.6
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	754.4	70.8	1032	15	US-10-353-445-2
3	639.4	61.9	1158	11	US-09-948-193-2
4	618.4	58.9	1553	10	US-09-916-780A-2
5	618.4	58.9	1553	10	US-09-880-107-3674
6	618.4	58.9	1553	11	US-09-948-193-8
7	618.4	58.9	1553	13	US-10-252-279-2
8	617.4	58.8	1032	13	US-10-097-554A-5
9	617.4	58.8	1032	15	US-10-161-403-58
10	617.4	58.8	1983	10	US-09-853-033-3
11	617.4	58.8	1983	10	US-09-853-033-5
12	617.4	58.8	1983	10	US-09-853-033-7
13	617.4	58.8	2346	15	US-10-353-445-4
14	617.4	58.8	2346	15	US-10-353-445-7
15	617.4	58.8	2346	15	US-10-353-445-8

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Sequence 48, Appli	19	281.6	26.8	3034	13	US-10-356-088-48
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Sequence 46, Appli	21	104.4	9.9	3597	13	US-10-190-435-46
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Sequence 60, Appli	23	95	9.0	3231	13	US-10-190-435-60
Sequence 84, Appli	24	95	9.0	3231	13	US-10-190-305A-84
Sequence 57, Appli	25	93	8.9	2742	13	US-10-190-435-57
Sequence 81, Appli	26	93	8.9	2742	13	US-10-190-305A-81
Sequence 59, Appli	27	91.4	8.7	4713	13	US-10-190-435-59
Sequence 83, Appli	28	91.4	8.7	4713	13	US-10-190-305A-83
Sequence 58, Appli	29	91.4	8.7	5184	13	US-10-190-435-58
Sequence 82, Appli	30	91.4	8.7	5184	13	US-10-190-305A-82
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Sequence 66, Appli	35	87.6	8.3	2568	13	US-09-967-464-66
Sequence 4, Appli	36	87	8.3	2400	13	US-10-228-063-4
Sequence 25, Appli	37	87	8.3	2478	13	US-10-228-063-25
Sequence 35, Appli	38	86.8	8.3	2078	13	US-10-307-047-35
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Sequence 2, Appli	40	86.6	8.2	3468	11	US-09-988-462-2
Sequence 4984, Ap	41	86	8.2	1506	15	US-10-156-761-4984
Sequence 7, Appli	42	86	8.2	4039	10	US-09-205-448-7
Sequence 65, Appli	43	85.6	8.2	2550	13	US-09-967-464-65
Sequence 57, Appli	44	85.4	8.1	3261	13	US-10-241-009-57
Sequence 57, Appli	45	85.4	8.1	3261	13	US-10-190-434B-57

ALIGNMENTS

RESULT 1

US-10-353-445-5
; Sequence 5, Application US/10353445
; Publication No. US2003011916A1
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. US2003011916A1e1 Method For The Integration Of Foreign D
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 5
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding mOre:FUpm, Cre from Bacteriophage P1 and
; OTHER INFORMATION: P1P from Saccharomyces, both maize preferred
; FEATURE: codons
; NAME/KEY: CDS
; LOCATION: (1)..(2346)

US-10-353-445-5

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Query Match      71.9%; Score 755; DB 15; Length 2346;
Best Local Similarity 83.4%; Pred. No. 4.6e-157;
Matches 857; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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; Sequence 2, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign D
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence encoding Cre protein from Bacteriophage
; OTHER INFORMATION: P1, maize preferred codons (moCRE)
US-10-353-445-2
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Query Match      71.8%; Score 754.4; DB 15; Length 1032;
Best Local Similarity 83.4%; Pred. No. 6.5e-157;
Matches 857; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGTGACCGTGACAGAACTGCGCCGCTGCGCGTGGACGGCAGCG 82
DB 2 TGTCCAACTGTCTACCGTTACAGAACTTCCGGCTCTTCCAGTGGACGGACGTCG 61

QY 83 ACAGGTGCGCAAGAACCTGTATGGACATGTTCCGCGACCGCGCGCTTCAGCGAGCA 142
DB 62 ATGAAGTCAGGAAGAACCTCATGGACATGTTCCGCGACAGGCAAGCGTTTCAGCGAGCA 121

QY 143 CTGTGAAGATGCTGTGAGCGTGTGCGGACGTGGCGCGCTGTGTCAGAGCTGAACAAC 202
DB 122 CTGTGAAGATGCTGTGAGCGTGTGCGGACGTGGCGCGCTGTGTCAGAGCTGAACAAC 181

QY 203 GCAAGTGGTTCCTCCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 262
DB 182 GGAAGTGGTTCCTCCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 241

QY 263 GCGGCTTGGCGTGAAGACCATCCAGACGACTGGGGCGAGTGAACATGCTGACCGCC 322
DB 242 GCGGGCTGGCAGTGAAGACCATCCAGACGACTGGGGCGAGTGAACATGCTTCAAGGC 301

QY 323 GCGAGGCTGTGCGCGCGCGCGCGAGCAGACGCGCTGAGCGCTGTGAGCGCGATCC 382
DB 302 GCTCCGGCTTCCCGCGCGCGCGAGCTGCGAACGCGCGCTGAGCGCTGTGAGCGCGATCA 361

QY 383 GCAAGGAGAACGTGGAGCGCGCGAGCGCGCCAGCGCCCTGGCGCTTCGAGCGCAACG 442
DB 362 GGAAGGAGAACGTGGAGCGCGCGAGCGCGCCAGCGCCCTGGCGCTTCGAGCGCAACG 421
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Qy 443 ACTTCGACCAAGTCCGAGCGCTGATGAGAAACAGCGACCGCTGCCAGGACATCCGCAACC 502
Db |||||
422 ATTTTCGACCAAGTCCGAGCGCTGATGAGAAACAGCGACAGGTGCCAGCAATTAGGAACC 481
Qy 503 TGGCCTTCCTGGGATCGCCTACCAACACCTGCTGGCATCGCGAGATCGCCCGCATCC 562
Db |||||
482 TGGCGTTCCCTGGGAATTGCAATACAAACGCTCCTCAGGATCGCGGAATTGCCCCGCAATC 541
Qy 563 GCGTGAAGGACATCAGCGCGACCGACCGCGCGCGCATGCTGATCCATCGCGCGCACCA 622
Db |||||
542 GCGTGAAGGACATTAGCGCGACCGACCGCGCGCGCATGCTGATCCATTTGGCAGGACCA 601
Qy 623 AGACCCCTGGTGAACCCCGCGCGTGGAGAAAGGCGCTGAGCCTGGCGGTGACCAAGCTGG 682
Db |||||
602 AGACGCTCGTTTCCACCGCGAGCGCTCGAAAGGCGCTCAGCGCTCGGAGTGACCAAGCTCG 661
Qy 683 TGGAGCGCTGATCAGCGGTGAGCGCGCTGGCGGACGACCCCAACACTACCTGTTCTGTC 742
Db |||||
662 TCGAACGCTGATCTCCGTTGTCGCGGCTCGGAGACGACCCCAACACTACCTGTTCTGTC 721
Qy 743 GCGTGGCGCAAGAACGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 802
Db |||||
722 GCGTGGCGCAAGAACGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 781
Qy 803 TGGAGGGGATCTTCGAGGCCACCCACCGCGCTGATCTACGGCGCGCAAGGACGACGCGCG 862
Db |||||
782 TGGAGGGTATTTTCGAGGCCACCCACCGCGCTGATCTACGGCGCGCAAGGATGACGCGGTC 841
Qy 863 AGCGCTACCTGGCTGGAGCGGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 922
Db |||||
842 AACGCTACCTGGCTGGAGCGGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 901
Qy 923 GCGCGCGGCTGAGCATCCCGAGATCATGACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
Db |||||
902 GCGCGGCTGTTTCCATCCCGAATCATGACAGCGGCTGGATGACGAACTGAACTG 961
Qy 983 TGATGAATACATCCGAACCTGGACAGCGAGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
Db |||||
962 TCATGAATACATTCGAACTTGACAGCGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1021
Qy 1043 ACGCGGAC 1050
Db |||||
1022 ATGGTGAC 1029
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RESULT 3

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US-09-948-193-2
; Sequence 2, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Ruley, H. Earl
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; TITLE OF INVENTION: Site-Specific Recombinases
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/230,690
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description: His6-NLS-Cre-MTS
US-09-948-193-2
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Query Match 60.9%; Score 639.4; DB 11; Length 1158;
Best Local Similarity 75.6%; Pred. No. 1.2e-131;
Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

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Qy 1 ATGCCCAAGAGAGAGAGAGTGAACAACCTCTGACCGTGACCAAGAACCTGCCCCGCC 60
Db |||||
61 ATGCCCAAGAGAGAGAGAGTGTCAATTTACTGACCGGTACACCAAAATTTGCGCTGCA 120
Qy 61 CTGCCCGTGACGCCACCGAGCAGAGGTGCGCAAGNACCTGATGACATGTTCCCGGAC 120
Db |||||
121 TTACCGGTCGATGCAACAGAGTGAAGTTCGCAAGAACCTGATGGACATGTTTCAAGGAT 180
Qy 121 CGCAGCGCTTCAGCGAGACACCTGGAAGATGCTGCTGAGCGTGTGCCCGCAGCTGGGCC 180
Db |||||
181 GCGCAGCGCTTCTGAGCATACCTGGAATAATGCTTCTGTCCGTTTGCCCGGTGCTGGCG 240
Qy 181 GCCTGTGTGAAGGTGAACAAACCGCAAGTGTTCCTCCCGCGAGGCGGAGGACGTCGCGG 240
Db |||||
241 GCATGTGTGCAAGTGAATAACCGGAAATGTTTCCCGCAGAACCTGAAGATGTTTCCGAT 300
Qy 241 TACTGTGTGCTGAGCGCGCGCGCGCTGGCGTGAAGACCATCCAGGACGACCTGGCC 300
Db |||||
301 TATCTTCTATATCTTCAAGGCGCGCGGTCTGGCAGTAAAACTATCCAGCAACATTTGGGC 360
Qy 301 CAGCTGAACATGCTGACCGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db |||||
361 CAGCTAACAATGCTTCACTCGTCCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 361 AGCCTGTGTGATGCGCGCGCATTCGCAAGGAGAACGTTGGAACCGCGCGCGCGCGCG 420
Db |||||
421 TCAGTGTGTATGCGCGGATCCGAAAGAAAAAGTGTGATCCCGGTGAACGTCGCAAAACAG 480
Qy 421 GCCTTGGCGCTTCGAGCGCACCGACTTCGACCAAGTGGCGGAGCTGATGGAGAACAGCG 480
Db |||||
481 GCTCTAGCGTTCGAAACGCGACTGATTCGACCGAGTTCGTTCACTCATGGAATAATAGCG 540
Qy 481 CGCTGCGAGACATCCGCAACCTGCGCTTCCTGGGCGATCGCTACCAACACCTGCTCGCG 540
Db |||||
541 CGCTGCGAGATATACGTAATCTGGCATTTCTGGGAGTTCGTTAACAACCTGTTAGCT 600
Qy 541 ATCGCGAGATTCGCGCGCATCCGCGTGAAGGACATCAGCCGCGCACCGCGCGCGCGCG 600
Db |||||
601 ATAGCGAAATTCGCGAGATCAGGTTAAAGATATCTCACGTACTGACGCTGGGAGAAATG 660
Qy 601 CTGATCCACATCGCGCGCACCAAGACCTGCTGAGGACCGCGCGCGTGGAGAGAGCGCTG 660
Db |||||
661 TTAATCCATATTCGCGAGAACGAAACGCTGTTAGCACCGCGAGGTGTAGAGAGAGCACTT 720
Qy 661 AGCCTGGCGCTGACCAAGCTGGAGCGCTGAGATCAGCGTGAAGCGCGCTGGCGGACGAC 720
Db |||||
721 AGCCTGGGGTAACTAACTGGTCGAGCGATGGAATTCGCTCTCTGCTGTAGCTGATGAT 780
Qy 721 CCCAACAACTACCTGTTCTGCGCGTGCAGAAACCGCGCTGGCGCGCGCGCGCGCGCG 780
Db |||||
781 CCGAATAACTACCTGTTTTCGCGGTTCAGAAAAATGTTGTGCGCGCGCATCTGCCACC 840
Qy 781 AGCAGCTGAGCACCGCGCGCGCTGGAGGCGATCTTGGAGGCGACCGACCGCTGATCTAC 840
Db |||||
841 AGCAGCTATCACTCGCGCGCTGGAGGAGTATTTTGAAGCACTCATCGATTCGATTTAC 900
Qy 841 GCGGCCAAGACGACAGCGCGCGCTACCTGCGCTGGAGCGCGCGCGCGCGCGCGCGGTG 900
Db |||||
901 GCGGCTAAGGATGACTCTGTCAGAGATACCTGGCGCTGGTCTGGACACAGTGGCGCGGTG 960
Qy 901 GCGCGCGCGCGCGACATGGCGCGCGCGCGGTGAGCATCCCGAGATCATGACGCGCGCG 960
Db |||||
961 GGAGCGCGCGAGATATGGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT 1020
Qy 961 GGTGGACCAACGTTGAACATGTTGATGAATCAATCCGCAACCTGGACAGCGGACCGCG 1020
Db |||||
1021 GGTGGACCAATGTTAAATATTTGTCATGAATATATATATCGTAACTGATGTAACAGGG 1080
Qy 1021 GCAATGTTGCGCTGCTGGAGGACGCGCA 1049
Db |||||
1081 GCAATGTTGCGCTGCTGGAGGATGGCGCA 1109
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RESULT 4
US-09-916-780A-2
; Sequence 2, Application US/09916780A
; Patent No. US20020124280A1
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; APPLICANT: Li, Yi O'Donnell, Colum Duan, Hui Wu, Yan McAvoy, Richard
; TITLE OF INVENTION: Methods for the Controlled, Automatic Excision of Heterologous DN
; TITLE OF INVENTION: Transgenic Plants and DNA-Excising Gene Cassettes for Use Therein
; FILE REFERENCE: 983933.0066
; CURRENT APPLICATION NUMBER: US/09/916,780A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,318
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Bacteriophage P1
US-09-916-780A-2

Query Match 58.9%; Score 618.4; DB 10; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACCTGCTGACCGTGCACAGAACCTGCCCGCCTCCCGTGGAGC 73
DB 477 AGTGTAAATGTCATTAATGCTGACCGTACACCAAAATTTGCCGTGCTATACCGTGCATG 536
QY 74 CCACGACGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCCAGCCCTTCA 133
DB 537 CAACGAGTGATGAGTTGCGAAGAACCTGATGACATGTTTCCAGGATCGCCAGCGTTT 596
QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGTGTGCCGACGCTGGCGCGCTGTCGACG 193
DB 597 CTGAGCATACCTGGAATGCTTCTGTCCTGTTGCCGCTGTCGGCGGCATGTTGCAAGT 656
QY 194 TGAACACCCAGTGTGTTCCCGCGACCGCGGAGCGCGGACTGCTGTGATGC 253
DB 657 TGAATACCCGAAATGTTTCCCGCGAAGCTGAAAGATGTTCCGATATCTTCTATATC 716
QY 254 TGACGCGCGCGGCTCGCGCTGAAGACCATCCAGCAGCACCTGGGCGAGCTGAACATGC 313
DB 717 TTACGCGCGCGTCTGCGAGTAAACTATCCAGCAACATTTGGCGCAGCTAAACATGC 776
QY 314 TGACCGCGAGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGATGC 373
DB 777 TTCATCTCGTCCGGGCTGCGACGCAAGTGAAGCAATGCTGTTTCACTGGTTATGC 836
QY 374 GCGCATCCGCAAGGAGAACCTGACGCGCGCGCGCGCGCGCGCGCGCGCTGCTTCG 433
DB 837 GCGGATCCGGAAGAAAGAAAGTGTGATGCGCGTGAACGTGCAAAACAGGCTTACGCTTCG 896
QY 434 AGCGACCGCACTTCGACAGGTGCGCGAGCTGATGAGAAACAGCAGCGCGCTGCCAGACA 493
DB 897 AACGCACTGATTTGCAACAGGTTCTGTTCACTCATGGAATAAGCATGCTGCCAGGATA 956
QY 494 TCCGCAACCTGGCTTCTGGGATGCTGCTACACACCTGCTGCGCATGCCAGATCG 553
DB 957 TACGTAATCTGGCAATTTCTGGGATGCTTAAACACCTGTTTACGTATAGCCGAAATG 1016
QY 554 CCGCATCCGCTGAAGGACATCAGCGCACCGCGCGCGCGCGCGCGCGCTGCTGATCCACATCG 613
DB 1017 CCAGATCAGGTTTAAAGATATCTCAGTACTGACGTTGGAGAAATGTTTATCCATATG 1076
QY 614 GCGCACCAAGACCTGTTGAGCACCGCGCGCGTGGAGAAAGCGCTGAGCCTGGCGCTGA 673
DB 1077 GCAGAACCAACCTGTTAGCACCGCAGGTGTAGAGAGGCACTTAGCCTGGGGTAA 1136
QY 674 CCAAGCTGGTGGAGCTGAGTTCAGCGTGAAGCGGCTGGCGAGCAACCCCAACACTACC 733

DB 1137 CTAAACTGGTGCAGCGATGGATTTCCGTCTCTGGTGTAGTGATGATCGAATAACTACC 1196
QY 734 TGTCTTCCCGCTGCGCAAGAACGCGTGGCGCGCCCGCCAGCGCCACCGAGCTGAGCA 793
DB 1197 TGTCTTCCCGCTGCGCAAGAACGCGTGGCGCGCCCGCCAGCGCTGATCAA 1256
QY 794 CCGGCGCTTGGAGGCACTTTCGAGGCGCACCGCGCTGATCTACGGCGCAAGGAGC 853
DB 1257 CTCGCGCGCTGGAAGGGATTTTGAAGCAACTCATCTGATTTACGCGCTAAGGATG 1316
QY 854 ACAGCGCGCAGCGCTACCTGGCGCTCGAGCGGCCACAGCGCGCGCGCGCGCGCGCG 913
DB 1317 ACTCTGGTCAAGATACCTGGCGCTGCTGACACAGTGGCGCTGTCGAGCGCGCGAG 1376
QY 914 ACATGCGCGCGCGCGCGTGAACATCCCGAGATCATGCGAGCGCGCGCGCTGCAACG 973
DB 1377 ATATGCGCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGCTGGCTGCAACATG 1436
QY 974 TGAACATCTGATGAACCTACATCCGCAACCTGACAGCGAGCGCGCGCATGTCGCGC 1033
DB 1437 TAAATATTGTCATGAACCTATATCCGTAACTGATAGTAGTGAACAGGGGCAATGGTGC 1496
QY 1034 TGCTGGAGGACGCGCA 1049
DB 1497 TGCTGAAGATGCGCA 1512

RESULT 5

US-09-880-107-3674
; Sequence 3674, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3674
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X03453
US-09-880-107-3674

Query Match 58.9%; Score 618.4; DB 10; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACCTGCTGACCGTGCACAGAACCTGCCCGCCTCCCGTGGAGC 73
DB 477 AGTGTAAATGTCATTAATGCTGACCGTACACCAAAATTTGCCGTGCTATACCGTGCATG 536
QY 74 CCACGACGAGGTGCGCAAGAACCTGATGACATGTTTCCGCGACCGCGAGCCCTTCA 133
DB 537 CAACGAGTGATGAGTTGCGAAGAACCTGATGACATGTTTCCAGGATCGCCAGCGCTTT 596
QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGTGTGCCGACGCTGGCGCGCTGTCGACG 193
DB 597 CTGAGCATACCTGGAATAATGCTTCTGTCCTGTTTGGCGTGTGGCGGCAATGGTGAAGT 656
QY 194 TGAACACCCAGTGTGTTCCCGCGCGAGCGCGCGAGGAGCGTGCAGCACTACTGCTGTGATC 253
DB 657 TGAATACCCGAAATGTTTCCCGCGAAGCTGAAAGTGTTCGATATCTTCTATATC 716

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QY 254 TGCAGCCCGCGGCTGCGCTGAGACCATCCAGCAGCACCTTGGCCAGCTGAACATGC 313
Db |||||
QY 717 TTCAGGCGCGGGTCTGGCAGTAAACATATCCAGCAACATTTGGGCGCAGCTAAACATGC 776
Db |||||
QY 314 TGCACCCCGCAGCGGGCTGCGCCCGCCCCACGACAGCAACGCGCTGAGCTGTGATGC 373
Db |||||
QY 777 TTCATCGTGGTCCGGGCTGCCAGCAACAGTGAAGCAATGCTGTTTCACTGGTTATGC 836
Db |||||
QY 374 GCGGCATCCGAAGAGAACTGTGAACCGCGCGAGCGCGCAAGCAAGCGCTTGGCCTTCG 433
Db |||||
QY 837 GCGGCATCCGAAGAGAAACGTTGATGCGCGTGAACGTTGCAAAACAGCGCTTAGCGTTGC 896
Db |||||
QY 434 AGCGACCGACTTCGACAGAGTGGCAGCCTGATGGAGAGAGAGAGAGAGAGAGAGAG 493
Db |||||
QY 897 AACGCATGATTTTCGACAGAGTTTGTTCACTCATGGAAGATAGCGATCGCTGCCAGGATA 956
Db |||||
QY 494 TCCGCAACCTTGGCCCTTCTCGGGCATCGCTCAACACACCTCTCGCATGCGCCAGATCG 553
Db |||||
QY 957 TAGGTATCTGGCATTTCTGGGATTTGCTTATACACCCCTGTACGTATAGCCGAATTCG 1016
Db |||||
QY 554 CCGGCATCCGGTGAAGAACTATAGCGCCACCGAGCGCGCGCGCATGCTGATCCACATCG 613
Db |||||
QY 1017 CCAGGATCAGGGTTAAAGATATCTCAGTACTGACCGGTGGAGAAATGTTAATCCATATG 1076
Db |||||
QY 614 GCGCAGCAAGACCTTGGTGAAGACCGCGCGGTGGAGAGAGCGCTGAGCTGGCGTGA 673
Db |||||
QY 1077 GCAGAACGAAACCGCTGTTAGCACCGCAGGTGTAGAGAGAGCGACTTAGCGCTGGGGTAA 1136
Db |||||
QY 674 CCAAGCTGGTGGAGCGCTGAGCTGAGCGCTGAGCGCGTGGCGAGACCCCAACAACTACC 733
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QY 1137 CTAACTGGTTCAGCGATGGATTTCCGTTCTGTGTAGCTGATGATCCGATTAACCTACC 1196
Db |||||
QY 734 TGTTCTGCGCGTCCGAAGAACCGCGGTGGCGCGCCCGCCAGCGCACAGCGAGCTGAGCA 793
Db |||||
QY 1197 TGTTTTCGCGGTGAGAAAAATGGTGTGCGCGCCATCTGCCAGCGAGCTATCAA 1256
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QY 854 ACAGCGCCAGCGCTACTCTGCGCTGGAGCGGCCACAGCGCGCGGTGGCGCGCGCGCG 913
Db |||||
QY 1317 ACTCTGTGAGAGATACTGGCTGTGTGGACACAGTGCCTGTGCGAGCGCGCGAG 1376
Db |||||
QY 914 ACATGGCGCGCGCGCGTGAAGCATCCCGAGATCATGCAAGCGCGCGGTGGACCAACG 973
Db |||||
QY 1377 ATATGGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGTGGACCAATG 1436
Db |||||
QY 974 TGAACATCGTGAATGATATCCGCAACCTGGACAGCGAGACCGCGCCATGTTGCGCC 1033
Db |||||
QY 1437 TAAATATGTCATGAATATATCCGTAACTTGGATGTGAAACAGGGGCAATGGTGGCGCC 1496
Db |||||
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RESULT 6

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US-09-948-193-8
; Sequence 8, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Ruley, H. Earl
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; TITLE OF INVENTION: Site-Specific Recombinases
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; PRIOR FILING DATE: 2001-09-07
; PRIOR FILING DATE: 60/230,690
; NUMBER OF SEQ ID NOS: 21
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; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Bacteriophage P1
; FEATURE:
; OTHER INFORMATION: Description: gene encoding Cre recombinase
US-09-948-193-8
```

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Query Match 58.9%; Score 618.4; DB 11; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;
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QY 14 AGAGGAGGTGAGCAACCTCTGACCGTGACCGTGACCGAGAACCTGCGCGCGCTGCCGTGAAGC 73
Db |||||
QY 477 AGTGTAAATGTCGAATTTACTGACCGGTACACCAAAATTTGCTGCAATACCGGTGATG 536
Db |||||
QY 74 CCACCGAGCAGAGGTGCGCAAGAACTGATGATGACATGTTCCGCGAGCCGCGCGCTTCA 133
Db |||||
QY 537 CAACGAGTGTAGGTTCGCAAGAACCTGATGACATGTTTCAGGGATCGCGCGCTTTT 596
Db |||||
QY 134 GCGAGCACACCTGGAAGATGCTGCTGAGCGTGTGCCGAGCTGGCGCGCTGGTGAAGC 193
Db |||||
QY 597 CTGAGCATACCTGGAAAAATGCTTCTGTCCGTTTGGCGGTCTGGCGGCAATGTCGCAAGT 656
Db |||||
QY 194 TGAACAAACCGCAAGTGGTTCCTCCCGAGCCCGAGGACGTCGCGCACTACTGCTGTACC 253
Db |||||
QY 657 TGAATAACCGGAATAGTTTCCCGCAGAACCTGAAGATGTTTCGCAATATCTTCTATATC 716
Db |||||
QY 254 TGCAGGCGCGCGCTGGCGTGAAGAACCATCCAGCAGCACTGGGGCCAGCTGAACATGC 313
Db |||||
QY 717 TTGAGCGCGCGGTCTGGCAGTAAACATATCCAGCAACATTTGGGCGAGCTAAACATGC 776
Db |||||
QY 314 TGCACCGCGCAGCGCGCTGCCCCCGCCAGCAGCAACCGCGTGGAGCTTGGTGTATGC 373
Db |||||
QY 777 TCCATCGTGGTCCGGCTGCCACGCAAGTGAAGCAATGCTGTTCACTGGTGTATGC 836
Db |||||
QY 374 GCGCATCCGCAAGGAGAGCTGAGCGCGCGAGCGCGCAAGCGCGCTTGGCCTTCG 433
Db |||||
QY 837 GCGCGATCCGAAAGAAACGTTGATGCGCGTGAACGTTGCAAAACAGCGCTTAGCGTTCG 896
Db |||||
QY 434 AGCGCACCGACTTCGACCGAGTGGCAGCTGATGGAGACAGCGACGCGCTGCCAGACA 493
Db |||||
QY 897 AACGCATGATTTTCGACAGAGTTTCTGCTCATGGAAGATAGCGATCGCTGCCAGGATA 956
Db |||||
QY 494 TCCGCAACCTTGGCCCTTCTGCGCATCGCTTAAACACCTTGTGCGCATCGCGAGATCG 553
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QY 957 TAGGTATCTGGCATTTCTGGGATTTGCTTATACACCCCTGTACGTATAGCCGAATTCG 1016
Db |||||
QY 554 CCGCATCCGGTGAAGAGCATGAGCGCGCACCGCGCGCGCGCGCTGCTGATCCACATCG 613
Db |||||
QY 1017 CCAGGATCAGGGTTAAAGATATCTCAGTACTGACCGGTGGAGAAATGTTAATCCATATG 1076
Db |||||
QY 614 GCGCAGCAAGACCTTGGTGAAGACCGCGCGGTGGAGAGAGCGCTGAGCTGGCGTGA 673
Db |||||
QY 1077 GCAGAACGAAACCGCTGTTAGCACCGCAGGTGTAGAGAGAGCGACTTAGCGCTGGGGTAA 1136
Db |||||
QY 674 CCAAGCTGGTGGAGCGCTGAGTCAAGCGCGTGGCGCGCTGGCGAGACCCCAACAACTACC 733
Db |||||
QY 1137 CTAACTGGTTCGAGCGATGGATTTCCGTTCTGTGTAGCTGATGATCCGATTAACCTACC 1196
Db |||||
QY 734 TGTTCTGCGCGTCCGAAGAACCGCGGTGGCGCGCCCGCCAGCGCACAGCGAGCTGAGCA 793
Db |||||
QY 1197 TGTTTTCGCGGTGAGAAAAATGGTGTGCGCGCCATCTGCCAGCGAGCTATCAA 1256
Db |||||
QY 794 CCGCGCGCTTGGAGGCGATCTTCGAGCGCACCGCGCTGGAGAGAGCGCTGAGCTGGCGTGA 853
Db |||||
QY 1257 CTCGCGCGCTGGAAGGATTTTGAAGCAACTCATCGATTTAGTTTTCGCGCGCTAAGGATG 1316
Db |||||
QY 854 ACAGCGCCAGCGCTACTCTGCGCTGGAGCGGCCACAGCGCGCGGTGGCGCGCGCGCG 913
Db |||||
QY 1317 ACTCTGTGAGAGATACTGGCTGTGTGGACACAGTGCCTGTGCGAGCGCGCGAG 1376
Db |||||
QY 914 ACATGGCGCGCGCGCGTGAAGCATCCCGAGATCATGCAAGCGCGCGGTGGACCAACG 973
Db |||||
QY 1377 ATATGGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGTGGACCAATG 1436
Db |||||
QY 974 TGAACATCGTGAATGATATCCGCAACCTGGACAGCGAGACCGCGCCATGTTGCGCC 1033
Db |||||
QY 1437 TAAATATGTCATGAATATATCCGTAACTTGGATGTGAAACAGGGGCAATGGTGGCGCC 1496
Db |||||
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QY	914	ACATGGCCCGCGCGCGTGAAGATCCCGAGATCATGCGAGCGCGGCTGGACCAACG	973
Db	1377	ATATGGCCCGCGCGTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATG	1436
QY	974	TGAACATCGTGTGAACATACATCCGCAACCTGGACACGAGACCGCGGCCCATGGTGGGCC	1033
Db	1437	TAAATATTGATGAACATATCCGTAACCTGGATAGTAGAAACAGGGGCAATGGTGGGCC	
QY	1034	TGCTGGAGGACGGCGA	1049
Db	1497	TGCTGGAAGATGGCGA	1512

RESULT 7

US-10-252-279-2

; Sequence 2, Application US/10252279

; Publication No. US20030190746A1

; GENERAL INFORMATION:

; APPLICANT: Xiao, Xiao

; APPLICANT: Xiao, Xiao

; TITLE OF INVENTION: GENE EXPRESSION CONTROL SYSTEM AND ITS USE IN RECOMBINANT

; TITLE OF INVENTION: CELL LINES

; FILE REFERENCE: 020059

; CURRENT APPLICATION NUMBER: US/10/252,279

; CURRENT FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: 60/369,987

; PRIOR FILING DATE: 2002-04-04

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1553

; TYPE: DNA

; ORGANISM: Bacteriophage P1

US-10-252-279-2

Query Match	58.9%;	Score 618.4;	DB 13;	Length 1553;
Best Local Similarity	74.8%;	Pred. No. 5.1e-127;		
Matches	775;	Conservative 0;	Mismatches 261;	Indels 0; Gaps 0;
QY	14	AGAGGAGGTGAGCAACCTGCTGACCGTGACACGAAACCTGCCCGCCTGCCCGTGGACG	73	
Db	477	AGTGTAAATCTCAATTTATCTGACCGTACACCAAAATTTGCCCTGCAATACCGTTCGATG	536	
QY	74	CCACCAGCGAGGTGCGAAGAACCTGATGGACATGTTCCGCGACGCGCACAGCCCTTCA	133	
Db	537	CAACGAGTGTAGGTTTCGAAGAACCTGTATGGACATGTTTCAGGGATCGCCAGCGGTTTT	596	
QY	134	GCAGACACACCTGGAAGATGCTGTGAGCGTGTGCCGAGCTGGCGCGCCTGTGTGCAAGC	193	
Db	597	CTGAGCATACCTGAAAAATGCTTCTGTCCGTTTGCCTGGTCTGGCGCGCATGTTGCAAGT	656	
QY	194	TGAACAACCGCAAGTGTTCCTCCGCGAGCCCGAGGACGTGCGCACTACTGCTGTACCC	253	
Db	657	TGAATAACCGAAATGTTTCCCGCAGAACCTGAAGATGTTTCGCGATTTATCTTCTATATC	716	
QY	254	TGACGGCCCGCGCTCGCGTGAAGACCATCGACGACACTCGGCGCAGCTGAACTATGC	313	
Db	717	TTACGGCGCGCGTCTGSCAGTAAAAACTATCCAGCAACATTTGGCGCCAGCTAAACATGC	776	
QY	314	TGCACCGCCGACGCGGCTGCCCGCCACCGGACAGCAACGCGTGAGCTGTGTATGC	373	
Db	777	TTCATCGTCTGTCGGGCTGCCACGACCAAGTGAAGCAATGCTGTTTCACTGTGTTATGC	836	
QY	374	GCCGCATCCGCAAGGAGAACTGGAAGCGCGCGAGCGGCCAAGCAGGCGCCTTGGCCTTCG	433	
Db	837	GGCGATCCGAAAGAAACGTTGATGCGCGTGAACGTGCAAAACAGGCTCTACGGTTCG	896	
QY	434	AGCGCACCGACTTCGACACAGGTGGCGAGCTCATGTGGAAACAGGACCGCGTCCGAGACA	493	
Db	897	AACGCACCTGATTTTCGACAGGTTGTTCACTCATGGAATAAGCGATCGCTGCCAGATA	956	
QY	494	TCCGCAACCTCGCTTCCTGGGCATCGCCTTCAACAACCTGCTGGCATTCGCCAGATCG	553	

Db	957	TACGTAATCTGGCAATTCCTGGGGAATTCCTATTAACACCCCTGTTACGTATAGCCGAATTCG	1016
Qy	554	CCGCGATCCGCGTGAAGGACATCAGCCGACCGACCGCGCGCGCGATCTGATCCACATCG	613
Db	1017	CCAGGATCAGGGTTAAAGATATCTCACGTACTCACGGTGGGAGAAATGTTAATCCATATTC	1076
Qy	614	GC CGCACCAAGACCTTGTTGAGCACACCGCGCGCTGGAGAGGCCCTCAGACCTGGGCGTGA	673
Db	1077	GCAGAAACGAAACCGCTGGTTAGCACCGCAGGTGTAGAGAAAGGCACCTTAGCCTCGGGGTAA	1136
Qy	674	CCAAGCTGCTGGAGCGCTGGATCAGCGTGTAGCGCGCTGGCGGACGACCCCAACAACTACC	733
Db	1137	CTAAACTGGTTCGAGCGATGGATTCCTCTCTGTTAGTGTATGATCCGATTAACCTACC	1196
Qy	734	TGTTCTGCGCGTGC GCGAAGAACCGCGTGC GCGCCGCCCAAGCGCACACAGCCAGCTGAGCA	793
Db	1197	TGTTTTTCGCGGTTCAGAAAAATGCTGTTGCCGCGCCATCTGCCACAGCAGCTATCAA	1256
Qy	794	CCGCGGCGCTGGAGGGCACTCTTCGAGGCCACCCACCGCCTGATCTAGCGCGCCAGAGACG	855
Db	1257	CTCGCGCCCTTGGAAAGGATTTTTTGAAGCAACTCATCGATTGATTTACGGCGCTAAAGGATG	1316
Qy	854	ACAGCGCCACGAGCTACTCTGCCCTGGAGCGGCGCACAGCGCCGCGTGGCGCGCCCGCGCG	913
Db	1317	ACTCTGGTCAGATATACCTGGCCCTGGTCTGTGACACAGTGC CGGTCTCGAGCCCGCGAG	1376
Qy	914	ACATGCGCCGCGCGCGCTGAGCATCCCCGAGATCATGCAAGCGCGCGGTGGACCAACG	973
Db	1377	ATATGCGCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATG	1436
Qy	974	TGAACATCTGTATGAACATACATCCGCAACTCTGACAGCGAGACCGCGGCCCATGTTGCGCC	1033
Db	1437	TAAATATTGTCTGAATATATCCGTAACCTGGATAGTGAACAGGGGGCAATGTTGCGCC	1496
Qy	1034	TGCTGGAGGACGGCGA 1049	
Db	1497	TGCTGGAGATGGCGA 1512	

RESULT 8

US-10-097-554A-5

; Sequence 5, Application US/10097554A

; Publication No. US20030170642A1

; GENERAL INFORMATION:

; APPLICANT: Jeremy Scot Caldwell

; APPLICANT: Sumit K. Chanda

; APPLICANT: Nikunj V. Somia

; APPLICANT: John B. Hogenesch

; APPLICANT: Michael P. Cooke

; APPLICANT: Pedro Aza-Blanc

; TITLE OF INVENTION: IDENTIFICATION OF CELLULAR TARGETS FOR BIOLOGICALLY ACTIVE

; FILE REFERENCE: 38417-1312

; CURRENT APPLICATION NUMBER: US/10/097,554A

; CURRENT FILING DATE: 2002-07-09

; PRIOR APPLICATION NUMBER: 60/275,266

; PRIOR FILING DATE: 2001-03-12

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1032

; TYPE: DNA

; ORGANISM: Escherichia coli

; FEATURE: 5

; NAME/KEY: CDS

; LOCATION: (1)...(1032)

; OTHER INFORMATION: nucleotide sequence encoding Cre recombinase

US-10-097-554A-5

Query Match	58.8%	Score 617.4;	DB 13;	Length 1032;
Best Local Similarity	75.1%	Pred. No. 8.6e-127;		
Matches 771;	Conservative 0;	Mismatches 256;	Indels 0;	Gaps 0;

Qy 23 TGAGCAACCTGCTGACCGTGCACCAAGCAACCTGCCCGCCCTCGCGTGGAGCGCCACGACGCG 82

Db	2	TGTCCAATTTACTGACCGGTACACCAAAATTTGCTGCAATTACCGGTCCGATGCAACGAGTG	61
Qy	83	ACGAGGTGCGCAAGAACTGATGGACATGTTTCCGCGACCGCCAGCGCTTCAGCGAGCACA	142
Db	62	ATGAGGTTCGCAAGAACTGATGACATGTTTCAGGGATCGCAGCGGTTTTCTGAGCATAT	121
Qy	143	CCTGGAGATCTCTGTGAGCGTGTGCGCAGCTGGCGCGCTGTGTGCAAGCTGAACAACC	202
Db	122	CCTGGAAAACTCTTCTGTCTCTTTCGCGGTGTTGGCGGCATGGTGCAGTTGAATAACC	181
Qy	203	GCAAGTGGTTCCCGCGCAGCCCGAGACGTGCGGCACTACTGCTGTACTTCAGGCGCC	262
Db	182	GGAATGGTTTTCCGCGAGAACTTGAAGATGTTCCGATTAATCTTCTATATCTTCAGGCGC	241
Qy	263	GCAGCTTCGGCGTGAAGAACCATTCAGCAGACCACTGGGCGAGCTGAACATGTGTGACCGCC	322
Db	242	GCAGTCTGCAGTAATAAATATCAGCAACATTTGGGCCAGCTAAACATGCTTCACTGTC	301
Qy	323	GCAGCGCTCCCGCGCCCAAGCAGCAGCAACAGCGGTGAGCGTGGTATGCGCGCGCAATCC	382
Db	302	GGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTCACTGGTTATGCGGGGATCC	361
Qy	383	GCAAGGAGAACTGGAGCGCGCGAGCGCGCAAGCAGCGCCCTGGCCTTCGAGCGCACCG	442
Db	362	GAAAGAAAACGTTGATGCGCGGTGAACGTGCAAAACAGGCTCTACGCTTCGAAACGCACTG	421
Qy	443	ACTTCGACCAAGTGGCAGCGCTGATGAGAAACAGCAGCGCTGCCAGGACATCCGCAACC	502
Db	422	ATTTTCGACCAAGTTCGTTCACTCATGGAATAAGGATCGCTGCCAGATATAGTAATC	481
Qy	503	TGGCTTCTTGGGATCGCTTAAACACCTCTGTGCGGATCGCGAGATCGCCGCAATCC	562
Db	482	TGGCATTTCTGGGATTTGCTTTAACAACCTGTTACGTATAGCGCAAAATGCCAGGATCA	541
Qy	563	GCGTGAGGACATCAGCGGACCAAGCGCGCGCATGCTGATCCACATCGGCGCGACCA	622
Db	542	GGGTAAAGATATCTCAGCTACTACCGTGGGAGAAATGTTAATCCATATTGCGAGACGA	601
Qy	623	AGACCTCTGTGAGCACCGCGCGTGGAGAAAGGCCCTGAGCCTGGCGGTGACCAAGCTGG	682
Db	602	AAACGCTGGTTAGCACCGCAGGTGTAGAAAGGCACCTAGCCTGGGGTAACTAACTGG	661
Qy	683	TGAGCGCTGGATCAGCGTAGCGCGGTGGCGACGACCCCAACAACTACCTGTTCTGCC	742
Db	662	TCGAGCGATGGATTTCCGTTCTCTGGTGTAGCTGATGATCCGAATACTACCTGTTTGGC	721
Qy	743	GCCTGCGCAGAACGGCGTGGCGCCCGCCAGCGCACAGCCCACTGAGCAACCGGGGCC	802
Db	722	GGGTGAGAAAAATGGTGTTCGCGCGCATCTGCGCACGACGACCTATCAACTCGCGCCC	781
Qy	803	TGGAGGCGATCTTCGAGGCGCAACCAACGCGCTGATCTACGGCGCGCAAGACGACGCGCC	862
Db	782	TGGAAGGATTTTGAAGCACTCATCGATTGATTTACGGCGCTAAGATGACTCTGGTC	841
Qy	863	AGCGCTACCTGGCGTGGAGCGGCAACAGCGCCGCGTGGGCGCGCCCGGACATGGCCC	922
Db	842	AGAGATACCTGGCGCTGGTCTGGACACAGTGCCTGTTCGAGCGCGCGAGATATGGCCC	901
Qy	923	GGCGCGCGTGGACATCCCGAGATCATGAGCGCGCGCGCTGGACCAAGTGAACATCG	982
Db	902	GCCTGGAGTTTCAATACCGGAGATCATGAAGCTGGTGGCTGGACCAATGTAAATATG	961
Qy	983	TGATGAACATACCTCGCAACTGGACAGCAGACCGCGCGCATCTGGTGGCGCTCTGGAGG	1042
Db	962	TCATGAACATATACCGTAACTTGGATGATGAACAGGGGCAATGGTGGCGCTCTGGAAG	1021
Qy	1043	ACGGCGA	1049
Db	1022	ATGGCGA	1028

RESULT 9

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US-10-161-403-58
; Sequence 58, Application US/10161403
; Publication No. US2003019104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1032)
; OTHER INFORMATION: nucleotide sequence encoding
US-10-161-403-58

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Query Match	58.8%	Score 617.4	DB 15	Length 1032	
Best local Similarity	75.1%	Pred. No. 8.6e-127			
Matches	771	Conservative 0	Mismatches 256	Indels 0	Gaps 0
Qy	23	TGAGCAACCTGCTGACCGTGACACAGAACTGCCCGCCCTGCCCGTGAGCGCCACCAAGC	82		
Db	2	TGTCCAATTTACTGACCGGTACACAAATTTGCTGCAATACCGGTGATGACACGAGTG	61		
Qy	83	ACGAGGTGCGCAAGAACTGATGCATGTTCCGCGACCGCCAGGCGCTTCAGCGGACACA	142		
Db	62	ATGAGGTTCCGAGAACCCTGATGCAATGTTCAGGATCGCCAGGCGTTCTTGAGCAT	121		
Qy	143	CCTGGAAAGATGCTGTGAGCGTGTCCGCGAGCTGGCGCGCTGGTGCAAGCTGAACAACC	202		
Db	122	CCTGGAAATGCTTCTGTCCGTTTGGCGGTGCTGGCGGCGATGCTGCAAGTTGAATAACC	181		
Qy	203	GCAAGTGGTTTCCCGCGAGCCGAGAGCGTGCGGACTACCTGCTTACCTTCAGCGCCC	262		
Db	182	GGAAATGGTTTCCCGCAGAACCTGAGATGTTCCGCAATATCTTATATCTTCAGGCGC	241		
Qy	263	GGCGCTGGCGGTGAAGACCATCCAGCACCTTGGGCCAGCTGAACATGCTGCACCGCC	322		
Db	242	GCGETTGGCGAGTAAAACTATCCAGCAATTTGGCCAGCTAAACATGCTTCATGTC	301		
Qy	323	GCACGCGCTGCCCGCCCGCCAGCGACAGCAACCGCGTGAGCTGTGTATGCGCGCGATCC	382		
Db	302	GTGCCGGCTGCCACGACCAAGTGAAGCAATGCTGTTTCACTGGTATTGCGCGGATCC	361		
Qy	383	GCAAGAGAAACGTGGACGCGCGGCGCGCCAAAGCAGGCGCTTGGCGCTTCGACGCGACCG	442		
Db	362	GAAAGAAAACGTTGATGCGGTGAACGTGCAAAACAGGCTCTAGCGTTTGAACGCACTG	421		
Qy	443	ACTTCGACAGGTGGCGACGCTGATGGAGAACAGCGACCGGTGCCAGGACATCCGAAACC	502		
Db	422	ATTTCAGCAGGTTCTGTCACTCATGGAAAAATAGCGATCGCTGCCAGGATATACGTAATC	481		
Qy	503	TGSCCTTCTGGGCATGCGCTACAACACCTCTGCGCATCGCCGAGATGCGCCGATCC	562		
Db	482	TGCAATTCCTGGGATTTGCTTATAACACCCCTGTACGTATAGCCGGAATTTGCCAGATCA	541		
Qy	563	GGGTGAAGACATCAGCCGACCGAGCGGCGCGCATGTGTTACCACTATCGGCGCACCA	622		

542	GGGTTAAAGATATCTCACTGACTGACGGTGGGGAATGTTAATCCATAATTGGCAGAACGA	601
Qy		
623	AGACCCCTGGTGTAGCACCGCCGGGTGAGAAGGCCCTGAGCCTGGGGCGTGACCAAGCTGG	682
Db		
602	AAACGCTGGTTAGCACCGCAGGTGTAGAAGGCATTAGCCTGGGGGTAACTAACTGG	661
Qy		
683	TGGAGCCTGGATCAGCGTGAGCGGTGGCCGACGACCCCAACAACTACCTGTTCTGGCC	742
Db		
662	TCGAGCGATGGATTTCGGTCTCTGGTGTAGCTGATGATCCGAATACTACCTGTTTGGCC	721
Qy		
743	CGCTGCCAAGAACGGGTGGCCGCCCGCCAGCCACGACCGAGCTAGCACCCGGGCCCC	802
Db		
722	GGGTCAAGAAAAATGTGTTTCCGCGCCATCTGCCACCGCCAGCTATCAACTCGCGCCC	781
Qy		
803	TGGAGGCGATCTTTCGAGGCCACCCACCGCCTGATCTACGGCGCCCAAGACGACAGCGGCC	862
Db		
782	TGGAAGGGATTTTGAAGCACTCATCGATTGATTACGGCGCTAAGATGACTCTGGTC	841
Qy		
863	AGCGCTACCTGGCCTGGAGCGGCCACAGCGCCCGCGTGGCGCGGCCCGGACATGGCCCC	922
Db		
842	AGAGATACCTGGCCTGGTCTTGGAACACAGTGCCTGTTCGGAGCGCGCGAGATATGGCCC	901
Qy		
923	GGCCCGCGTGAACATCCCGAGATCATGAGCGCGCGCGCTGGACCAACGTGAACATCG	982
Db		
902	GCCTGGAGTTTCAATACCGGAGATCATGAAGCTGGTGGCTGGACCAATGTAAATATTG	961
Qy		
983	TGATGAACCTACATCCGCAACTCTGGACAGCAGACCGCGCCATGGTCGCGCTGCTGGAGG	1042
Db		
962	TCATGACTATATCCGTAACTTGATAGTAGAACAGGGGCAATGGTGGCGCTGCTGGAG	1021
Qy		
1043	ACGGCGA	1049
Db		
1022	ATGGCGA	1028
Qy		

RESIST. 10

```

US-09-853-033-3
; Sequence 3, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1983)
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
; OTHER INFORMATION: Homosapiens-Bacteriophage P1
US-09-853-033-3

```

RESULT 11

US-09-853-033-5 ; Sequence 5, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, PIERRE

APPLICANT: METZGER, DANIEL
TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
FILE REFERENCE: 065691/0222
CURRENT APPLICATION NUMBER: US/09/853,033
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: FR 00/12570
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1983
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1983)
OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
OTHER INFORMATION: Homosapiens-Bacteriophage P1
US-09-853-033-5

Query Match 58.8%; Score 617.4; DB 10; Length 1983;
Best Local Similarity 75.1%; Pred. No. 8.3e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 23 TGAGCAACCTGCTGACCGTGACCAACCTGCGCCCTGCGCGGAGCCACCGG 82
DB 2 TGTCAAATTACTGACCGTACCAAAATTGCTGCTACCTACCGGTGATGCAAGAGT 61
QY 83 ACAGGTGCGCAAGAACCTGATGGACATGTTCCGGACCGCCAGGCGCTTCAGCGAGCACA 142
DB 62 ATGAGGTTCCGAAGAACCTGATGGACATGTTCCAGGATCGCCAGGCGTTTCTGAGCATA 121
QY 143 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTCATCGAGCGCGGCTGGAACCAATCG 202
DB 122 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTCATCGAGCGCGGCTGGAACCAATCG 181
QY 203 GCAAGTGGTTCCCGCGAGCGCGAGGAGCTGCGGAGCTACCTGCTGCTGAGCGGCC 262
DB 182 GGAATGGTTTCCCGCGAGAACCTGGAAGATGTTCCGGAATATCTTCTATATCTTCAGGGCG 241
QY 263 GCGGCTGCGCGTGAAGACATCCAGACACCTGCGGCGAGCTGGAACATGCTGCAACCGCC 322
DB 242 GCGGTCTGCGAGTAAACTATCCAGACACATTTGGCGCAGCTAAACATGCTTCACTGTC 301
QY 323 GCAGGCGCTGCGCGCGCCAGCAGCAGCAAGCGCGTGTGATGCGCGCGCATCC 382
DB 302 GGTCCGGGTGCGCAGCAAGTGAAGTGTCTTCACTGCTTATGCGGCGGATCC 361
QY 383 GCAAGGAGACGTGAGCGCGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 442
DB 362 GAAAGAAACGTTGATCGCGGTGAACGTGCAAAACAGGCTCTAGCGTTTCGAACGCACTG 421
QY 443 ACTTCGACGAGTGGCGAGCGCTGTGAGAGAACAGCGACCGGCTGCCAGGACATCCGCAACC 502
DB 422 ATTTGACGACGAGTTGTTCACTCATGGAATAGGATGCTGCGCAGGATATACGTAATC 481
QY 503 TGGCGCTTCCTGGGATCGCTTACAAACACCTGCTGCGCATCGCGGAGATCGCGCGCATCC 562
DB 482 TGGCATTTCTGGGATGCTTATAACACCTGTTACGTTATAGCGGAAATTCGAGGATCA 541
QY 563 GCGTGAAGGACATCAGCGCGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 622
DB 542 GGGTTAAAGATATCTCAAGTACTGACCGTGGGAGAAATGTTAATCCATATTCGCGAAGCA 601
QY 623 AGACCTGCTGAGCACCGCGCGTGGAGAGGCGCTGAGCGCTGGCGGTGACCAAGCTGG 682
DB 602 AAACGCTGGTGAACCGAGGTGAGAGAGGCGCTTAGCGCTGGGGGTAACTAAACTGG 661
QY 683 TGGAGCGCTGATCAGCGGTGAGCGGCGTGGCGGAGCGACCCCAACAACTACCTGTTCTGCC 742
DB 662 TCGAGCGATGATTTCCGCTCTCTGCTGTAGCTGATGATCCGAAATACCTACCTGTTTGGC 721

QY 743 GCGTGGCAAGAACGGCGTGGCGCGCCCGCCAGCGCCACCGAGCCAGCTGAGCACCCCGGCCC 802
DB 722 GGGTCAGAAAAAATGTTGTCGGCGCCATCTGCCACCGAGCTATCAACTCGCGCCC 781
QY 803 TGGAGGGCATCTTCGAGGCGCACCCACCGCTGATCTAGGCGCCCAAGGACGACAGCGGC 862
DB 782 TGGAGGGATTTTGAAGCACTCATGATTGATTACGGCGCTAAGGATGACTCTGGTC 841
QY 863 AGCGTACCTGCGCTGGAGCGCCACAGCGCGCGGCTGGCGCGCCCGCGGACATGCGCC 922
DB 842 AGAGATACCTGCGCTGGTCTGGACACAGTGCCTGTCGGAGCGCGGAGATATGCGCC 901
QY 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGGCTGGAACCAACGTAACATCG 982
DB 902 GCGCTGGAGTTTCAATATCCGGAGATCATGCAAGCTGTGGTGGACCAATGTAATATG 961
QY 983 TGATGAATACATCCGCAACCTGGAGCGGACGAGCGCGCCATGTCGCGCTGCTGAGG 1042
DB 962 TCATGAATATATCTGTAACCTGGATAGTGAACAGGGGCAATGCTGCGCTGCTGGAAG 1021
QY 1043 ACGGCGA 1049
DB 1022 ATGGCGA 1028
RESULT 12
US-09-853-033-7
; Sequence 7, Application US/09853033
; Patent No. US2002010068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1983)
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
; OTHER INFORMATION: Homosapiens-Bacteriophage P1
US-09-853-033-7

Query Match 58.8%; Score 617.4; DB 10; Length 1983;
Best Local Similarity 75.1%; Pred. No. 8.3e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 23 TGAGCAACCTGCTGACCGTGACCAACCTGCGCCCTGCGCGGAGCCACCGG 82
DB 2 TGTCAAATTACTGACCGTACCAAAATTGCTGCTACCTACCGGTGATGCAAGAGT 61
QY 83 ACAGGTGCGCAAGAACCTGATGGACATGTTCCGGACCGCCAGGCGCTTCAGCGAGCACA 142
DB 62 ATGAGGTTCCGAAGAACCTGATGGACATGTTCCAGGATCGCCAGGCGTTTCTGAGCATA 121
QY 143 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTCATCGAGCGCGGCTGGAACCAAC 202
DB 122 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTCATCGAGCGCGGCTGGAACCAAC 181
QY 203 GCAAGTGGTTCCCGCGAGCGCGGAGGAGCTGCGGAGCTACCTGCTGCTGAGCGGCC 262
DB 182 GGAATGGTTTCCCGCGAGAACCTGGAAGATGTTCCGGAATATCTTCTATATCTTCAGGCGC 241
QY 263 GCGGCTGCGCGTGAAGAACCAATCCAGCACCTGGGCGCAGCTGAACATGCTGCAACCGCC 322

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Db 242 GGGTCTGCGAGTAAATATCCAGCAACATTTGGCGCAGCTAAACATGCTTCATGTC 301
QY 323 GCAGCGCTGCCCGCCCGCCAGCAGCAACCGCGTGAGCCTGTGTGATGCGCCGCATCC 382
Db 302 GGTCCGGGTGCGCCAGCAGCAAGTGACAGCAATGCTTTCATGTTATGCGCGGATCC 361
QY 383 GCAAGGAGACGTGAGCGCGCGGAGCGCGCAAGAGCGCCTGGCCTTCGAGCGCAGCG 442
Db 362 GAAAGAAACGTTGATGCGCGTGAAACGTGCAAAACAGGCTCTAGCGTTGCAACGCACTG 421
QY 443 ACTTCGACAGGTGGCGCAGCCTGATGGAGAACAGCGACCGCTGCCAGGACATCCGCAACC 502
Db 422 ATTTCGACAGGTTCGTTCACTCATGGAATAAGGATGCTGCCAGGATATACGTAATC 481
QY 503 TGGCCTTCCTGGGATCGCTCAACACCTCTCGCATCGCCGAGATCGCCCGCATCC 562
Db 482 TGGCATTTCTGGGATTCGTTATAACACCTCTAGTATAGCCGAAATGCGCAGGATCA 541
QY 563 GGTGAAGACATCAGCGCACGAGCGCGCGCGCATGCTGATCCACATCGCGCGACCA 622
Db 542 GGGTTAAAGATATCTCACGTACTGACGCTGGGAGAAATGTTATCCATATTGGCAGAGCA 601
QY 623 AGACCTCGTGTAGCACCGCGCGGTGGAGAGCGCCTGAGCCTGGGCGTGACCAAGCTGG 682
Db 602 AAACGCTGTTAGCACCGCAGGCTGAGAGAGGCACTTAGCCTGGGGTAACTAACTGG 661
QY 683 TGGAGCGTGTGATCAGCGGTGAGCGCGGTGGCGACGACCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGTCCTCTGGTGTAGCTGATGATCCGAAATAACTACCTGTTTGGC 721
QY 743 GGTGCGCAAGACGCGCTGGCGCCCGCCAGCGCCACAGCGCAGTGTAGCACCAGCGGCC 802
Db 722 GGGTCAGAAAAAATGGTGTGCGCGCCATCTGCCACAGCAGCATCAACTCGCGGCC 781
QY 803 TGGAGGGATCTTCAGAGCCACCCACCGCTGATCTAGCGCGCAAGAGCAGACGCGGCC 862
Db 782 TGAAGGATTTTGAAGCACTCATGATGATTTAGCGGCTTAAGGATGACTCTGGTC 841
QY 863 AGCGCTACTGCGCTGGAGCGCCACAGCGCGCGCGGTGGCGCCCGCCGACATGGGCC 922
Db 842 AGAGATACCTGCGCTGGTCTGACACAGTGCCCGGTGCGAGCGCGCGAGATGGGCC 901
QY 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGGTGAGCAACGATGAAATCG 982
Db 902 GCGCTGAGATTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATG 961
QY 983 TGATGAATACATCCGCAACCTGGAGCAGCGAGCGCGCGCATGCTGCGCCTGCTGGAGG 1042
Db 962 TCATGAATATATCGTAACCTGGATAGTGAACAGGGGCAATGGTGGCCCTGCTGGAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028
```

RESULT 13

US-10-353-445-4

; Sequence 4, Application US/10353445

; Publication No. US20030119166A1

; GENERAL INFORMATION:

; APPLICANT: Baszczynski, Christopher L.

; APPLICANT: Lyszniak, Leszek A.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Guan, Xueni

; APPLICANT: Rao, Guru

; APPLICANT: Tagliani, Laura A.

; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA

; FILE REFERENCE: 5718-66 (amended listing)

; CURRENT APPLICATION NUMBER: US/10/353,445

; CURRENT FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: US/09/193,503B

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; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
; OTHER INFORMATION: sequence encoding a Cre:FLPm polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-10-353-445-4
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Query Match 58.8%; Score 617.4; DB 15; Length 2346;

Best Local Similarity 75.1%; Pred. No. 8.2e-127;

Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

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QY 23 TGAGCAACCTCTGACCGTGCCAGAACCTGCCCGCCCTGCCGTGGAGCCACCGACGC 82
Db 2 TGGCCAAATTTACTACCGGTACACCAAAATTTGCCCTGCATTACCGGTGCATGCAACGATG 61
QY 83 ACAGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCCAGCGCTTCAGCGAGCACA 142
Db 62 ATGAGGTTGCGAAGAACCTGATGACATGTTGAGGATCGCCAGCGGTTTCTGAGCATAT 121
QY 143 CCTGGAAGATGCTCTGAGCGTGTGCCGACGCTGGCGCGCTGGTGTGCAAGCTGAACAACC 202
Db 122 CCGTGGAAAATGCTTCTGTCGTTTGGCGGTGCTGGCGGCATGTGTCAAGTTGAATAACC 181
QY 203 GCAAGTGGTTCCTCCCGCAGCGCCGAGGACGTGCGGACTACTCTCTGTACTGTGAGGCCC 262
Db 182 GGAATAGTGTTCGCGAGAACCTGAAGATGTTCCGATATATCTTCTATATCTTCAGGGCG 241
QY 263 GCGGCTGGCGGTGAGAACCATCCAGCAGCATCTGGCGCGCTGGTGTGCAAGCTGTGACGCC 322
Db 242 GCGGTCTGGCAGTAAAACTATCCAGCAACATTTGGCGCCAGCTAAAATGCTTTCATGCTC 301
QY 323 GCAGCGGCTGCCCCCGCCAGCGACAGCAACCGCGTGAGCCTGGTGTGATGCGCGCATCC 382
Db 302 GGTCCGGCTGCCACGACCAAGTGACAGCAATGCTGTTCACTGTTTATGCGCGGATCC 361
QY 383 GCAAGGAGAGCGTGGAGCGCGCGGAGCGCGCAAGAGGCGCTGGCCTTCGAGCGCACCG 442
Db 362 GAAAGAAAACGTTGATGCGCGGTGAACGTGCAAAACAGGCTCTAGCGTTTCGAAACGCACTG 421
QY 443 ACTTCGACAGGTGCGCAGCGCTGATGGAGAACAGCGACCGCTGCCAGGACATCCGCAACC 502
Db 422 ATTTCGACAGGTTCGTTCACTCATGGAATAAGGATGCTGCCAGGATATACGTAATC 481
QY 503 TGGCCTTCCTGGGATCGCTCAACACCTCTGCGCATCGCCGAGATCGCCCGCATCC 562
Db 482 TGGCATTTCTGGGATTCGTTATAACACCTCTGTTACGTATAGCCGAAATGCGCAGGATCA 541
QY 563 GCGTGAAGACATCAGCGCGCACCGAGCGCGCGCATGCTGATCCACATCGCGCGACCA 622
Db 542 GGGTTAAAGATATCTCACGTACTGACGCTGGGAGAAATGTTAAATCCATATTGGCAGAGCA 601
QY 623 AGACCTCGTGTAGCACCGCGCGGTGGAGAGCGCCTGAGCCTGGGCGTGACCAAGCTGG 682
Db 602 AAACGCTGTTAGCACCGCAGGCTGAGAGAGGCACTTAGCCTGGGGTAACTAACTGG 661
QY 683 TGGAGCGCTGTGATCAGCGGTGAGCGCGGTGGCGACGACCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGTCCTCTGGTGTAGCTGATGATCCGAAATAACTACCTGTTTGGC 721
QY 743 GGTGCGCAAGACGCGCTGGCGCCCGCCAGCGCCACAGCGCAGTGTAGCACCAGCGGCC 802
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Db 722 GGGTCAGAAAAATGGTGTTCGCGCCATCTGCCACGAGCCAGCTATCAACTCGGCCCC 781
Qy 803 TGGAGGGATCTTCGAGGCCACCCAGCCTGATCTACCGGCGCAAGGACGACGCGCC 862
Db 782 TGGAAAGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGGATGACTCTGGTC 841
Qy 863 AGCGCTACCTGGCGTGGAGCGCCACAGCGCCGCGTGGCGCGCCCGCGACATGGCCC 922
Db 842 AGAGATACCTGGCTGGTCTGGACACAGTGCCTGGTTCGAGCGCGCGAGATATGGCCC 901
Qy 923 GCGCGCGGTGAGCATCCCCAGATCATCAGCGCGCGCGCTGGACCAACGTTGAACATCG 982
Db 902 GCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
Qy 983 TGATGAATACATCCGAACTTGGACAGGACCGCGGCCCATGTTGGCCCTGCTGGAGG 1042
Db 962 TCATGAATATATCCGTAACTTGGATAGTGAACAGGGGCAATGTTGGCCCTGCTGGAAG 1021
Qy 1043 ACGCGCA 1049
Db 1022 ATGGCGA 1028

RESULT 14

US-10-353-445-7
; Sequence 7, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding a Cre:FLP polypeptide, Cre from
; OTHER INFORMATION: Bacteriophage P1 and FLP from Saccharomyces
US-10-353-445-7

Query Match 58.8%; Score 617.4; DB 15; Length 2346;
Best Local Similarity 75.1%; Pred. No. 8.2e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 23 TGAGCAACCTGCTGACCGTGCACAGAACCTCGCCGCGCTCGCCGTCGAGCCACCGCG 82
Db 2 TGGCCAATTTACTGACCGTACACCAAAATTTGCTGATACCGGTGATGCAACAGATG 61
Qy 83 ACGAGGTGCGCAAGAACTGATGACATGTTTCCGCGACCGCGAGCCCTTCAGCGAGACA 142
Db 62 ATGAGGTTCGCAAGAACTGATGACATGTTTCCAGGATTCGCCAGCGCTTTTCGAGATA 121
Qy 143 CCTGGAAGATGCTGCTGAGCGTGTGCCGACGTGGCGCGCTGTTGCAAGCTGAACAACC 202

RESULT 15

US-10-353-445-8
; Sequence 8, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni

Db 122 CTTGAAAAATGCTTCTGTCCGTTTCCCGGTCTGTGGCGGCGCATGGTGAAGTTGAATAACC 181
Qy 203 GCAAGTGTGTCCCGCGAGAGCCGAGGAGCTGTGCGGAGCTTACCTGTGTACCTGCGAGGCC 262
Db 182 GGAATGTGTTCGCGCAAACTTGAAGATGTTCCGATATCTTCTATATCTTTCAGGCGC 241
Qy 263 GCGGCTGCGCGTGAAGACCATCCAGCAGACCTTGGCCAGCTGAACATGTGTGCAACGCC 322
Db 242 GCGGTCTGGCAGTAAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGCTTCATGTC 301
Qy 323 GCAGCGGCTGCGCGCGCCAGCAGACAGCGCGCTGAGCTGTGTGATGGCGCCGATCC 382
Db 302 GGTCCGGCTGCCAGCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 361
Qy 383 GCAAGGAAAGTGGAGCGCGCGCGAGCGCGCAAGCAGCGCTGTGCGCTTCGAGCGCACCG 442
Db 362 GAAAGAAAAGTGTGATGCCCGTGAACGTGCAAAACAGCTCTAGCGTTCGAAGCACTG 421
Qy 443 ACTTCGACAGGTGCGAGCCTGATGGAGAACAGCAGCGCTGCCAGACATCCGCAACC 502
Db 422 ATTTGCAACAGGTTCGTTCACTCATGGAATAAGCATCGCTGCCAGGATATACGTAATC 481
Qy 503 TGGCTTCTCGGCGATCGCCTACACACCTGCTGCGCATCGCGATCGCGAGATTCGCGCGATCC 562
Db 482 TGGCATTTCTGGGATTTCTTATAACACCTGTTACGTATAGCCGAAATTCGCGGATCA 541
Qy 563 CGGTGAAGGACATCAGCGCACCGCGCGCGCATGCTGATCCACATCCACATCCGCGCACCA 622
Db 542 GGGTTAAGATATCTCAGTACTGACGCTGGAGAAATGTTAATCCATATTTGGAGAAAGA 601
Qy 623 AGACCTGTGAGCACCGCGCGCTGGAGAGCGCTGAGCTGGCGGTGACCAAGCTGG 682
Db 602 AAACGCTGGTTAGCACCGCAGCTGTAGAGAAAGCATTAGCTGGGGTAACTAACTGG 661
Qy 683 TGGAGCGCTGATCAGGTGAGCGCGCTGGCGCAGCAGCCCAACAACTACCTGTTGTC 742
Db 662 TCGAGCGATGGATTTCCGTCTCTGCTGTAGTGTATGATCCGATAAATACTACCTGTTT 721
Qy 743 CGGTGCGCAAGACGGGTGCGCGCGCGCGCATGCTGATCTACGCGCGCAAGCAGACGCGCC 802
Db 722 GGGTCAGAAAAATGGTGTTCGCGCGCAATCTGCCAGCAGCTATCAACTCGCGGCC 781
Qy 803 TGGAGGCACTTTCAGGCGCACCCACCGCTGATCTACGCGCGCAAGCAGACGCGGCC 862
Db 782 TGGAAAGGATTTTGAAGCAACTCATCGATTGATTACGCGCTAAGATGACTCTGGTC 841
Qy 863 AGCGCTACCTGGCGTGGAGCGCGCACAGCGCGCGCTGGCGCGCGCGCGACATGGCCC 922
Db 842 AGAGATACCTGGCGTGGTCTGGACACAGTGCCTGTCCGAGCGCGCGAGATATGGCCC 901
Qy 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGCTGAGCCCAAGCAAGTGAACATCG 982
Db 902 GCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGAGCAATGTAATATTG 961
Qy 983 TGATGAATACATCCGCAACCTGGAACAGCAGCGCGCGCATGTTGTCGCTGCTGAGG 1042
Db 962 TCATGAATATATCCGTAACTTGGATAGTGAACAGGGGCAATGTTGCGCTGCTGGAAG 1021
Qy 1043 ACGCGCA 1049
Db 1022 ATGGCGA 1028

APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. US20030119166A1el Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/10/353,445
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/09/193,503B
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 2346
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
OTHER INFORMATION: from Bacteriophage P1
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2346)
US-10-353-445-8

Query Match 58.8%; Score 617.4; DB 15; Length 2346;

Best Local Similarity 75.1%; Pred. No. 8.2e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 23 TGAGCAACCTGCTACCGTGCACAGAACCTGCCGCGCCCTGCCGTGGAGCCACCGCG 82
Db 1316 TGGCCATTACTGACCGTACCCAAATTTGCGCTGCAATTACCGTGCATCAACGAGTG 1375
Qy 83 ACGAGGTGCGAAGAACCTGATGGACATGTTCCGCGACCGCCAGGCGCTTCAGCGAGCACA 142
Db 1376 ATGAGTTTCGCAAGAACCTGATGGACATGTTTCAGGATCGCCAGGCGTTTCTGAGCATA 1435
Qy 143 CCTGGAAGATGCTGCTGAGCGTGTGCCAGCTGGCGCGCTGGTGCAGCTGAACAC 202
Db 1436 CCTGGAATGCTTCTGTCCTGTTGCCGCTCGTGGCGGCGATGGTCAAGTTGAATAAC 1495
Qy 203 GCAAGTGGTTCGCCCGCGAGCGCGAGGACGTGCGGACTACCTGCTGTACCTGCAGGCGCC 262
Db 1496 GGAAATGGTTTCCGCGAGAACTGAAGATGTTCCGGATATCTTCTATATCTTCAGGCGC 1555
Qy 263 CGGCGCTGGCGGTGAAGAACCTCAGCAGACCTGGGCGAGCTGAAACATGCTGCACCGCC 322
Db 1556 CGGGTCTGGCAGTAAAAAATAATCCAGCAACATTTGGGCGAGCTAAACATGCTTCATCGTC 1615
Qy 323 GCAGGCGCTCGCGCGCCCGCGAGCGCGAGCGCGCTGGCGCTGGTGCATGGCGCGATCC 382
Db 1616 GGTCCGGCTGCCACGACCAAGTACAGCAATGCTGTCTTCACTATGCGCGGATCC 1675
Qy 383 GCAAGGAGAACGTGGAGCGCGCGCGAGCGCGAGCGCGCTGGCGCTTCGAGCGCACCG 442
Db 1676 GAAAGAAACGTTGATGCCCGGTGAACGTGCAAAACAGGCTCTAGCGTTTCGACGCACTG 1735
Qy 443 ACTTCGACCGGTGCGAGCGCTGATGGAGAACAGCGACCGCTGCCAGGACATCCGCAACC 502
Db 1736 ATTTTCGACCGGTTCGTTCACTCATGGAATAATAGCATCGCTGCCAGGATATACGTAATC 1795
Qy 503 TGGCCTTCCTGGGATCGCCTACAAACACCTGCTGGCATCGCGAGATGCGCCGCGATCC 562
Db 1796 TGGCATTTCTGGGATGCTTTATAACACCTGTTACGCTATAGCGGAAATTCGCGAGATCA 1855
Qy 563 GCGTGAAGGACATCAGCGCGACCGCGCGCGCATGCTGATCCACATCGCGCGCACCA 622

Db 1856 GGGTTAAAGATATCTCAGTACTGACGGTGGGAGATGTTAAATCCATATTGGGACAGACGA 1915
Qy 623 AGACCCCTGGTGGAGCACCGCGCGGTGGAGAAAGCCCTGAGCCTGGGCGTGACCAAGCTGG 682
Db 1916 AAACGCTGGTTAGCACCGCAGGTGTAGAGAAAGGCACTTAGCCTGGGGGTAACTAAACTGG 1975
Qy 683 TGGAGCGCTGGATCAGCGTGGAGCGGTGGCCGAGACCCGCAACAACTACTGTCTTCTGCC 742
Db 1976 TCGAGCGATGGAATTTCCGCTCTCTGGTGTAGCTGATGATCCGAATAACTACTGTCTTCTGCC 2035
Qy 743 GCGTGCCTCAAGAACGGCGTGGCGCCCGCCAGCGCCACCGCCAGCTGAGCACCCGCGGCC 802
Db 2036 GGGTCAGAAAAAATGGTGTGGCGGCCATCTGCCACCGCCAGCTATCAACTCGCGGCC 2095
Qy 803 TGGAGGCGCATCTTTCGAGGCCACCCAGCCGCTGATCTACGGCGGCCAAGAGCAGACGCGGCC 862
Db 2096 TGGAAAGGATTTTGAAGCAACTCATCGATTGATTTTACGGCGCTAAGGATGACTCTCTGTC 2155
Qy 863 AGCGCTACCTGGCTGGAGCGGCCACAGCGCCCGCTGGGCGCGCCCGCGGACATGGCCCC 922
Db 2156 AGAGATACCTGGCTGGTCTGGACACAGTCCCGTGTCCGAGCGCGCGAGATATGGCCC 2215
Qy 923 GCGCGCGCGTGAGCATCCCGAGATCATGAGCGCGCGCGCTGGACCAACGTGAACATCG 982
Db 2216 GCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 2275
Qy 983 TGATGAACATACATCCGCAACTCGGACAGCGAGACCGCGCGCATGGTGCCTCTGTGGAGG 1042
Db 2276 TCATGAACATATATCCGTAACTGGATAGTAGTGAACAGGGGCAATGGTGCCTCTGTGAG 2335
Qy 1043 ACGGCGA 1049
Db 2336 ATGGCGA 2342

Search completed: December 16, 2003, 05:43:24

Job time : 1949 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 01:24:58 ; Search time 2664 Seconds
(without alignments)
9579.467 Million cell updates/sec

Title: US-09-662-128A-1

Perfect score: 1050

Sequence: 1 atgcccaagaagaaggaa.....gocgtggaggagcgac 1050

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum-DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	37.1	688	12	BI651236 603298328
2	231	22.0	431	9	AW211323 603298328
3	181.2	17.3	563	12	BI650191 603296283
4	158.8	15.1	340	9	AW212478 603296283

C	5	150.6	14.3	338	9	AW211972	AW211972 uo79f01.x
	6	128.2	12.2	343	9	AW210918	AW210918 uo89c09.y
	7	86	8.2	836	12	BI556329	BI556329 603237448
C	8	84.4	8.0	822	29	CC405275	CC405275 PUHJX22TD
C	9	81.8	7.8	838	29	BZ728954	BZ728954 OGBDN92TM
	10	79.8	7.6	288	29	FR0013439	FR0013439 F_rubripe
C	11	75.6	7.2	925	29	CNS0091P	AL004689 Drosophil
	12	74.6	7.1	727	13	BQ483660	AL053013 Drosophil
	13	74.4	7.1	852	12	B1949774	BQ483660 WHB3511.B
	14	74.4	7.1	854	10	BF261766	BF261766 HV_CEA000
	15	73.4	7.0	706	29	BZ564057	BF261766 HV_CEA000
C	16	72	6.9	949	29	CNS031R8	BZ564057 pacs2-164
	17	72	6.9	1536	13	BQ064626	AL223901 Tetradon
	18	71	6.8	2598	11	AY103647	BQ064626 AGENCOURT
	19	70.8	6.7	779	14	CB642703	AY103647 Zea mays
C	20	70.6	6.7	1170	14	CD496623	CB642703 OSJNEB03A
	21	70.4	6.7	616	13	BQ779181	CD496623 CDA23-C11
	22	70.4	6.7	1204	29	BZ558963	BQ779181 946117E08
	23	70.4	6.7	1491	11	AY104431	BZ558963 pacs2-164
	24	70.2	6.7	759	14	CB643463	AY104431 Zea mays
	25	70.2	6.7	856	14	CB645086	CB643463 OSJNEB04C
	26	70.2	6.7	877	14	CB620195	CB645086 OSJNEB06J
	27	70.2	6.7	882	14	CB668745	CB620195 OSIEA05D
	28	69.8	6.6	616	29	CNS03VVH	CB668745 OSJNEA16L
	29	69.4	6.6	859	14	CB650537	AL262934 Tetradon
	30	69.4	6.6	907	14	CB650537	CB650537 OSJNEB15A
	31	69	6.6	624	13	BQ606324	CB650537 OSJNEB15A
	32	69	6.6	935	29	CNS006XX	BQ606324 BRY_2176
	33	69	6.6	1011	29	BZ563437	BQ606324 BRY_2176
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	37	68.6	6.5	789	14	CB623003	CB647898 OSJNEB11A
	38	68.6	6.5	789	14	CB623065	CB675225 OSJNEB10N
	39	68.6	6.5	792	14	CB623042	CB623003 OSIEA10G
	40	68.6	6.5	801	29	BZ532691	CB623065 OSIEA10I
	41	68.6	6.5	806	14	CB622999	CB623042 OSIEA10H
	42	68.6	6.5	812	14	CB625663	BZ532691 OGALJ67TC
	43	68.6	6.5	820	14	CB623063	CB622999 OSIEA10G
	44	68.6	6.5	838	14	CB622964	CB625663 OSIEA15B
	45	68.6	6.5	839	14	CB669047	CB623063 OSIEA10I
							CB622964 OSIEA10F
							CB669047 OSJNEB01E

ALIGNMENTS

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RESULT 1
BI651236
LOCUS      603298328F1 NCI_CGAP_Mam3 Mus musculus cdna clone IMAGE:5338806 5',
DEFINITION mRNA sequence.
ACCESSION  BI651236
VERSION     BI651236.1
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 688)
            NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgapbs-x@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LIML at:
            http://image.liml.gov
            Plate: LIML1860 row: h column: 07
            High quality sequence stop: 688.

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	FEATURES	SOURCE
1.	100% Cotton	USA
2.	Machine Washable	USA
3.	Soft Touch	USA
4.	Light Blue Color	USA
5.	Short Sleeve	USA
6.	V-Neckline	USA
7.	Regular Fit	USA
8.	Long Length	USA
9.	Easy Care	USA
10.	Durable Fabric	USA
11.	Comfortable	USA
12.	Stylish Design	USA
13.	High Quality	USA
14.	Good Value	USA
15.	Great Gift Idea	USA
16.	Perfect for All Seasons	USA
17.	Available in Multiple Colors	USA
18.	Can Be Worn as a Jacket or Sweater	USA
19.	Machine Dryable	USA
20.	Does Not Shrink	USA
21.	Does Not Fade	USA
22.	Does Not Wrinkle	USA
23.	Does Not Stretch	USA
24.	Does Not Pill	USA
25.	Does Not Tear	USA
26.	Does Not Stain	USA
27.	Does Not Odor	USA
28.	Does Not Itch	USA
29.	Does Not Irritate Skin	USA
30.	Does Not Cause Allergies	USA
31.	Does Not Contain Harmful Chemicals	USA
32.	Does Not Contain Lead	USA
33.	Does Not Contain Mercury	USA
34.	Does Not Contain Cadmium	USA
35.	Does Not Contain Nickel	USA
36.	Does Not Contain Copper	USA
37.	Does Not Contain Zinc	USA
38.	Does Not Contain Silver	USA
39.	Does Not Contain Gold	USA
40.	Does Not Contain Platinum	USA
41.	Does Not Contain Palladium	USA
42.	Does Not Contain Rhodium	USA
43.	Does Not Contain Iridium	USA
44.	Does Not Contain Ruthenium	USA
45.	Does Not Contain Cobalt	USA
46.	Does Not Contain Manganese	USA
47.	Does Not Contain Chromium	USA
48.	Does Not Contain Vanadium	USA
49.	Does Not Contain Niobium	USA
50.	Does Not Contain Tantalum	USA
51.	Does Not Contain Tin	USA
52.	Does Not Contain Antimony	USA
53.	Does Not Contain Bismuth	USA
54.	Does Not Contain Arsenic	USA
55.	Does Not Contain Selenium	USA
56.	Does Not Contain Tellurium	USA
57.	Does Not Contain Polonium	USA
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59.	Does Not Contain Francium	USA
60.	Does Not Contain Actinium	USA
61.	Does Not Contain Thorium	USA
62.	Does Not Contain Uranium	USA
63.	Does Not Contain Neptunium	USA
64.	Does Not Contain Plutonium	USA
65.	Does Not Contain Americium	USA
66.	Does Not Contain Curium	USA
67.	Does Not Contain Berkelium	USA
68.	Does Not Contain Californium	USA
69.	Does Not Contain Einsteinium	USA
70.	Does Not Contain Fermium	USA
71.	Does Not Contain Mendelevium	USA
72.	Does Not Contain Nobelium	USA
73.	Does Not Contain Lawrencium	USA
74.	Does Not Contain Rutherfordium	USA
75.	Does Not Contain Dubnium	USA
76.	Does Not Contain Seaborgium	USA
77.	Does Not Contain Bohrium	USA
78.	Does Not Contain Hassium	USA
79.	Does Not Contain Meitnerium	USA
80.	Does Not Contain Darmstadtium	USA
81.	Does Not Contain Roentgenium	USA
82.	Does Not Contain Copernicium	USA
83.	Does Not Contain Nihonium	USA
84.	Does Not Contain Flerovium	USA
85.	Does Not Contain Oganesson	USA
86.	Does Not Contain Tennessine	USA
87.	Does Not Contain Moscovium	USA
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89.	Does Not Contain Uue	USA
90.	Does Not Contain Uub	USA
91.	Does Not Contain Uuh	USA
92.	Does Not Contain Uus	USA
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/clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site1: Sall;
Site2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
22..37-43 (1999)."
180 a 158 c 177 g 173 t
BASE COUNT

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BASE COUNT	180 a	158 c	177 g	173 t
ORIGIN				

Query Match	37.1%	Score 390;	DB 12;
Best Local Similarity	74.8%	Pred. No. 4.8e-60;	
Matches 489;	Conservative	0;	Mismatches 165;
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			Gaps 0;

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Db	35	AGTGTGAATGTCCAATTCTGACCGTACACAAAAATTTGCCTGCATTACCGGTGCGATG	94
QY	74	CCACCAGCAGAGGTGCGCAAGAACCTGATGGACATGTTCCGGCAGCCGCCAGGCCTTCA	133
Db	95	CAACGAGTGATGAGGTTCCGAAGAACCTGATGACCATGTTTCAGGGATCGCCAGCGCGTTTT	154
QY	134	GCAGCACACCTGGAAAGATGCTGTAGCGCTGTGCCGACGTGGCGCGCCTGTGTGCAAGC	193
Db	155	CTGAGCATACTGGAAATGTTCTGTCCGTTTGC CGGTCGTGGCGCGCATGTGTGCAAGT	214
QY	194	TGAACAACCGAAAGTGTTCCTCCGCCGAGCCCGAGGACGTGC GCGACTACTGCTGTATCC	253
Db	215	TGAATACCGGAAATGTTTTCCCGCAGAACCTGAAGATGTTCCGGATATCTTCTATATC	274
QY	254	TGACGCCCGCGCGCTGGCGGTGAAGACCAATCCAGCAGCACCTGGGCCAGCTGAACATGC	313
Db	275	TTCAGGCGCGCGTGTGGCAGTAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGC	334
QY	314	TGCACCGCCGAGGGCGCTCCCGCCGCCAGCAGCAGCAAGCCGCTGAGCGCTGGTGATGC	373
Db	335	TTCATCGTCGGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGC	394

Qy	374	GCGCGATCCGCAAGGAGAACGTGGACGCCCGCGAGCGCGCCAAAGCAGGCGCTCGGCTTCG	433
Db	395	GGCGGATCCGAAAGAAACGTTGATGCCGGTGAACGTGCAAAACAGGCTCTACGCTTCG	454
Qy	434	AGCGCACCGACTTCGACCCAGGTGCGGAGCCTGATGGAGAACAGCGACCGCTGCCAGACA	493
Db	455	AACGCACGTGATTCGACCCAGGTTCTTCATCTATGNAATAAGCGATCGGTGCCAGGATA	514
Qy	494	TCGCGAACCTGGCGCTTCCTGGGGATCGCCTAACACACCTGCTGGCGATCGCCGAGATCG	553
Db	515	TACGTAATTCGGCATTTCTGGGGATTGCTTTATAACACCCCTGTTACGCTATAGCCGAATTG	574
Qy	554	CCGCGATCCGCGTGAAGGACATCAGCGGCACCGCGCGCGCGCATGCTGATCCACATCG	613
Db	575	CCAGGATCAGGTTAAAGATATCTCAGTACTGACGGTGGGAGANTGTTATCCATATTG	634
Qy	614	GCGCGACCAAGACCTTGGTGAGACCGCGCGGTGGAGAGGCGCTTGAGCGTGG	667
Db	635	GCAGAACGAAACCGCTGGTTAGCACCGCGAGGTGTAGAGAGGCACATTAGCCTCG	688

[illegible]

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL COMMENT
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similar to SW:RECR_BBP1 P06956 RECOMBINASE CRE. [1] ;, mRNA
sequence.
AW211323
AW211323.1 GI:6517271
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Other ESTs: uo79f01.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

MGI:1029213
Seq primer: -40RP from Gibco
High quality sequence stop: 279.

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

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/_clone_lib="NCI CGAP Mam3"
/_note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NciI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia peng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22: 37-43 (1999)."
22. 37-43 (1999).

BASE COUNT	118 a	101 c	111 g	101 t
ORIGIN	118 a	101 c	111 g	101 t

Query Match	22.0%;	Score 231;	DB 9;	Length 431;
Best Local Similarity	71.0%;	Pred. No. 1e-31;		
Matches 306;	Conservative	0;	Mismatches 125;	Indels 0;
				Gaps 0;

197	QY	ACAACGCGAAGTGGTTCCCGCGGAGCCCGAGGACGTCGCGACTACCTGCTGTACTCTGC	256
	Db	1 ATAACCGGAAATGGTTCCCGCAGAACCTGAAGATGTCGCGATTATCTTATATCTTC	60
257	QY	AGGCGCGCGCTGGCGGTGAAGACCATCCAGCACCTGCGGCAGCTGAACATGCTGC	316
	Db	61 AGGCGCGCGTCTGGCAGTAAAACTATCCAGCACATTTGGGCAGCTAAACATGCTTC	120
317	QY	ACGCGCGAGCGCTGCCCCGCCAGCGA CAGCAACGCCGTGAGCTGTGATCGCC	376
	Db	121 ATCGTGGTGGCGGCTGCCAGCACCAAGTGA CAGCAATGCTTTCACTGGTTATGCGC	180
377	QY	GCATCGCAAGGAGAACGTGGACGGCGGACGCCAAGCAGAGCCCTGGCTTCGAGC	436
	Db	181 GGATCCGAAAGAAACAGTTGATCGCGTGAACGTGC AAAACAGAGCTTAGCGCTTGAAC	240
437	QY	GCACGCACTTCGACAGGTGGCGACCTGTATGGAGAA CAGCGACCGCTGCCAGGACATCC	496
	Db	241 GCACGTGATTTCCAGCAGGTTGGTTCACTCATGGAAAAATAGCCATCGCTGCCAGGATATAC	300
497	QY	GCAACCTGCGCCTTCTCGGCGATCGCCTACAACACCCCTGTCGCGATCGCCAGATCGCC	556

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Db      301  GTATCTGGCATTTCTGGGATTGCTTTAATACACCGGTAACCTATATAGCCGGAATGCCA 360
Qy      557  GCATCCCGCTGAAGGACATCAGCGCACCGACCGCGCGCGCATCTGATCCACATCGGCC 616
Db      361  GGATCAGGGTAAAGATATCTCACCGCTTCAGCGTGGGAGAAATGGTAATCCATATTGGGA 420
Qy      617  GCACCAAGACC 627
Db      421  GAAGCGAACC 431

RESULT 3
LOCUS   BI650191                563 bp    mRNA    linear    EST 12-SEP-2001
DEFINITION 603296288F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5336853 5',
mRNA sequence.
ACCESSION BI650191
VERSION   BI650191.1 GI:15564427
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 563)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LJM11855 row: f column: 22
          High quality sequence stop: 563.
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              /tissue_type="tumor, gross tissue"
              /dev_stage="10 months"
              /lab_host="DH10B"
              /clone_lib="NCI_CGAP_Mam3"
              /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali;
              Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
              Library constructed by Life Technologies. Investigators
              providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
              Reference for transgenic model: Xu et al., Nature Genetics
              22, 37-43 (1999)."
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BASE COUNT 143 a 133 c 149 g 138 t
ORIGIN
Query Match 17.3%; Score 181.2; DB 12; Length 563;
Best Local Similarity 76.6%; Pred. No. 7.7e-23;
Matches 222; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy      760  GTGGCCCGCCCGCAGCGCCAGCGAGCTGAGCACCAGCGGCGCTGGAGGGCATCTTCGAG 819
Db      1  GTTGGCGGCATCTGCCACAGCGCAGCTATCACTCGCGCCCTGGAGGGATTTTGAA 60
Qy      820  GCCACCCACCGCTGATCTACGGGCCAAGGACGACGCGCCAGCGCTACCTGGCGCTGG 879
Db      61  GCAACTCATCGATTGATTACGGGCGCTAAGGATGACTCTGGTCAGAGATACCTGGCGCTGG 120
Qy      880  AGCGGCGCACAGCGCGCGGTGGGCGCGCGCCGACATGCGCCCGCGGGGTGAGCATC 939
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Db      121  TCTGGACACAGTGCCTGTCGGAGCGCGGAGATATGCGCCGCTGAGTTTCAATA 180
Qy      940  CCGGAGATCATGAGCGCGCGCTGGACCAACGTAACATCTGTGATGAACTACATCCGC 999
Db      181  CCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTGTCATGAATATATCCGT 240
Qy      1000  AACCTGACAGCGAGACCGCGCCATGGTGGCGCTGCTGGAGGACGCGCA 1049
Db      241  AACCTGATAGTGAACAGGCGCAATGGTGGCGCTGCTGGAGATGGCGA 290

RESULT 4
LOCUS   AW212478/c            340 bp    mRNA    linear    EST 03-DEC-1999
DEFINITION uo89c09.x1 NCI_CGAP Mam3 Mus musculus cDNA clone IMAGE:2649712 3',
similar to SW:RECR_BPPI P06956 RECOMBINASE CRE. [1] ;, mRNA
sequence.
ACCESSION AW212478
VERSION   AW212478.1 GI:6518565
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 340)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished
COMMENT   Other ESTs: uo89c09.Y1
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          MGI:1030164
          Seq primer: -40UP from Gibco
          High quality sequence stop: 158.
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              /dev_stage="10 months"
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              Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
              Library constructed by Life Technologies. Investigators
              providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
              Reference for transgenic model: Xu et al., Nature Genetics
              22, 37-43 (1999)."
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BASE COUNT 75 a 100 c 79 g 86 t
ORIGIN
Query Match 15.1%; Score 158.8; DB 9; Length 340;
Best Local Similarity 76.0%; Pred. No. 7.2e-19;
Matches 196; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy      792  CACCGCGCGCTCGAGGGCATCTTCGAGGCCACCCACGCGCTGATCTACGCGCCCAAGGA 851
Db      293  CAACTCGCGCTCGAAGGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGGA 234
Qy      852  CGACAGGGCGCAGCGCTACCTGCGCTGGAGCGCCACAGCGCCGCGGTGGCGCGCGCGCG 911
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Db      233  TGATTCTGGTCAGAGATACCTGGCTGCTGTGGACACAGTGCCCGCTGTCGGAGCCGCGG 174
QY      912  CGACATGCCCGCGCGCGGTGAGCATCCCGAGATCATGACGCGCGCGGTGACCAA 971
Db      173  AGATATGCCCGCGCGGTGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGTGGACAA 114
QY      972  CQTGAACATCGTGATGAACCTACATCCGCAACTGACAGCGAGACCGGCGCATGGTCG 1031
Db      113  TGTAAATATTGTCATGAACCTATATCCGTAACTGGATAGTGAACAGGGGCAATGGTCG 54
QY      1032  CCTGCTGAGGACGGCGA 1049
Db      53  CTGCTGGAAGATGGCGA 36

RESULT 5
AW211972/c
LOCUS      AW211972      338 bp      mRNA      linear      EST 03-DEC-1999
DEFINITION uo79f01.x1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:2648761 3,
            similar to SW:RECR_BPP1 P06956 RECOMBINASE CRE. [1] ;, mRNA
ACCESSION  AW211972
VERSION     AW211972.1 GI:6517961
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 338)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Other ESTs: uo79f01.y1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

MGI:1029213
Seq primer: -40UP from Gibco
High quality sequence stop: 151.
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            /clone="IMAGE:2648761"
            /tissue_type="tumor, gross tissue"
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            Site 2: Noti; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigators
            providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
            Reference for transgenic model: Xu et al., Nature Genetics
            22, 37-43 (1999)."
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BASE COUNT 78 a 93 c 82 g 85 t

Query Match 14.3%; Score 150.6; DB 9; Length 338;

Best Local Similarity 76.7%; Pred. No. 2.1e-17;

Matches 197; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 793 ACCCGGCCCTGGAGGCGATCTTCGAGCGCACCCACCGCTGATCTACGGCGCCAGGAC 852

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Db      292  ACTCGCGCCCTGGAGGGAT-TTCTAAGCCACTCATCGATTGATTTACGGCGCTAAGAT 234
QY      853  GACAGCGCCAGCAGCTACCTGGCTGGAGCGGCCACAGCGCCCGCTGGCGCGCCCGC 912
Db      233  GACTTTGGTCAGAGATACCTGGCTGGCTGTCGGACACAGTGCCTGTGCGGAGCCGCTTA 174
QY      913  GACATGCGCGCGCGCGGTGAGCATCCCGAGATCATGACGCGCGCGGTGACCAAC 972
Db      173  CATATGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAAT 114
QY      973  GTGAACATCGTGATGAACCTACATCCGCAACTGACAGCGAGACCGGCGCATGGTCGC 1032
Db      113  GTAAATATTGTCATGAACCTATATCCGTAACTGGATAGTGAACAGGGGCAATGGTCGC 54
QY      1033  CTGCTGAGGACGGCGA 1049
Db      53  CTGCTGGAAGATGGCGA 37

RESULT 6
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DEFINITION uo89c09.y1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:2649712 5,
            similar to SW:RECR_BPP1 P06956 RECOMBINASE CRE. [1] ;, mRNA
ACCESSION  AW210918
VERSION     AW210918.1 GI:6516858
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 343)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Other ESTs: uo89c09.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

MGI:1030164
Seq primer: -40RP from Gibco
High quality sequence stop: 222.
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            /clone="IMAGE:2649712"
            /tissue_type="tumor, gross tissue"
            /dev_stage="10 months"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Mam3"
            /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
            Site 2: Noti; Cloned unidirectionally. Primer: Oligo dt.
            Library constructed by Life Technologies. Investigators
            providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
            Reference for transgenic model: Xu et al., Nature Genetics
            22, 37-43 (1999)."
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BASE COUNT 95 a 77 c 85 g 84 t

Query Match 12.2%; Score 128.2; DB 9; Length 343;

Best Local Similarity 66.5%; Pred. No. 2.1e-13;

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Matches 228; Conservative 0; Mismatches 110; Indels 5; Gaps 3;
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QY 379 ATCCGCAAGGAGAACTGTGACCGCGCGAGCGCGCAAGCAGCGCTTGCCTTCGAGCGC 438
Db 62 ATCCGAAAGAAACGTTGATCGCGGTGAACGTGCAGAACAGGCTTAGCGTTCCAGCGC 121
QY 439 ACCGACTTCGACAGGTGCGAGCTGTATGAGAGAACAGCGACCGCTGCAGACATCCGC 498
Db 122 ACTGATTTTC-ACCAGGTTGGTTCACTCATGGAATAAGCATCGCTGCAGGATATAGT 180
QY 499 AACCTGGCTTCTCGGCA-TGCGCTACAAACCCCTGCTGCATCGCGGAGATCGCGG 557
Db 181 AATCTGGCATTTTGGGGGATTTGCTTATAACACCCCTGTACGTATAGCGGAAATGNCAG 240
QY 558 CATCGCG- -TGAAAGGACATCAGCGCGCAGCGCGCGCGCATGCTGATCCACATCGG 614
Db 241 GATCCANGGGTTAAAGATTCATTACGCTTGAGCTGGAGAAAATGTTAAATCCATATGTG 300
QY 615 CGGACCAAGACCTCGGTGAGCACCGCGCGGCGTGAGAGGCC 657
Db 301 CAGAAACAAACCCCTGTTTACCCCGCAGTGTAGAAAAGGCC 343

RESULT 7
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LOCUS 603237448F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5290619 5',
DEFINITION mRNA sequence.
ACCESSION BI556329
VERSION BI556329.1 GI:15443643
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 836)
NIH-MGC http://www.ncbi.nlm.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11734 row: p column: 12
High quality sequence stop: 790.
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/tissue_type="tumor, gross tissue"
/dev_stages="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
```

BASE COUNT 208 a 224 g 186 t
 ORIGIN

```

Query Match 8.2%; Score 86; DB 12; Length 836;
Best Local Similarity 77.6%; Pred. No. 7.4e-06;
Matches 104; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 916 ATGGCCCGCGCGGCTGAGCATCCCGAGATCATGAGCGCGCGGTGACCAACCTG 975
Db 160 ATGCCAGGCGTTTCTGAGCATACCGAGATCATGCAAGCTGTGGCTGGACCAATGA 219
QY 976 AACATCGTGAATACTACATCCGCAACCTGACAGCAGAGACCGCGCCATGTCGCTG 1035
Db 220 AATATTGTGATGAATATATCCGTAACTCGTATAGTGAACAGGGGCAATGTCGCGCTG 279
QY 1036 CTGAGGACGCGGA 1049
Db 280 CTGGAAGATGCGGA 293

RESULT 8
CC405275 822 bp DNA linear GSS 19-MAY-2003
LOCUS PUHJX22TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBta468C20,
DEFINITION genomic survey sequence.
ACCESSION CC405275
VERSION CC405275.1 GI:30885365
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 822)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick
, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
Maize Genomics Consortium
Unpublished
Other_GSSs: PUHJX22TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
source 1..822
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBta468C20"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"
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BASE COUNT 132 a 263 c 275 g 152 t
 ORIGIN

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Query Match 8.0%; Score 84.4; DB 29; Length 822;
Best Local Similarity 50.2%; Pred. No. 1.4e-05;
Matches 270; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 54 GCCCGCGCTGCCGCTGGAGCGCCACGAGCGAGGTGGCGAAGAACTGATGACATGTT 113
Db 680 GGCGCGTGGCTGCACGAGGCCACCGCGGACGAGG-----AGTACTGAGTACGTGTC 627
QY 114 CCGCGACCGCCAGCGCTTACGAGCAGCACCTCGAAGATGCTCTGAGCGTGTGCCGCG 173
Db 626 CCGGAAACGCGAGGAGTTCGGCGGATCGGCTGCTCGTGTCTCGAGTTCCTCTGGGACAA 567
QY 174 CTGGCGCGCTGCTGCAAGCTGAACACCAACGCAAGTGTTCCTCCGCGAGCCCGAGGACGT 233
Db 566 CAAGTACGCGCGCTGCAGGTGCTCTCTCCAAAGCGCTCTCTCGCGCGCGCGCGCG 507
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BASE COUNT	72 a	70 c	70 g	73 t	3 others
ORIGIN	/clone="122014bG11"				
Query Match	7.6%	Score 79.8	DB 29	Length 288	
Best Local Similarity	80.9%	Pred. No. 8.5e-05			
Matches	93	Conservative	0	Mismatches 22	Indels 0
Gaps	0				
Qy	1	ATGCCCAAGAAAGAGAGAGTGCAGCAACTGCTGACCGGTGCACCAAGAACTCGCCGCC 60			
Db	54	ATGCCCAAGAGAGAGAGAGTGTCCAAATTACTGACCGGTACACCAAAATTGCTGTGCA 113			
Qy	61	CTGCCCGTGGACGCCACAGCAGCGAGGTGCGCAAGAACTGTATGGACATGTTTCC 115			
Db	114	TTACCGGTGCATGCAACAGAGTGTATGAGTTCGCCAAGAACTGTATGGACATGTTTC 168			
RESULT 11					
CNS0091P/c	925 bp DNA linear GSS 03-JUN-1999				
LOCUS	Drosophila melanogaster genome survey sequence TET3 end of BAC #				
DEFINITION	BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL053013				
VERSION	AL053013.1 GI:4934461				
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
AUTHORS	1 (bases 1 to 925)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
	Determination of this BAC end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeogawa and Aaron Mammoser in Pieter de Jong's laboratory at Kazutoyo Ooeogawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial, EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .				
FEATURES	Location/Qualifiers				
source	1..925				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:7227"				
	/clone="BACR19D16"				
	/clone_lib="RPCI-98"				
	/notes="end : TET3"				
BASE COUNT	120 a	61 c	61 g	172 t	511 others
ORIGIN					
Query Match	7.2%	Score 75.6	DB 29	Length 925	
Best Local Similarity	14.1%	Pred. No. 0.00053			
Matches	52	Conservative 184	Mismatches 134	Indels 0	Gaps 0
Qy	552	CGCCCGCATCGCGTGAAGGACATCAGCCACCGCGCGCGCATGCTGATCCACAT 611			
Db	924	SBGSCGSCGSRBSCSSSSMSTSSSSBSCSSSSBSSSTSSSSSSSSSGSSSS 865			
Qy	612	CGGCCGCAACAAGACCTGTGTGACACCGCGCGCGGTGGAGAAGCCCTGAGCCTGGCGGT 671			

and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 135 a 274 c 212 g 106 t
ORIGIN

Query Match 7.1%; Score 74.6; DB 13; Length 727;
Best Local Similarity 45.4%; Pred. No. 0.00079;
Matches 269; Conservative 0; Mismatches 324; Indels 0; Gaps 0;
QY 454 GTGCGCAGCTGATGAGAGACAGGACCGCTGCCAGGACATCCGCAACCTGCGCTTCCTG 513
Db 81 GTCTGCTACGGCGTGTGTCGCAACAACTCCCGCGGCAACAGAGTGTGAGCTTAC 140
QY 514 GCATCGCTACAAACACCTGCTGCGCATCGCGAGATCGCCGATCGGCTGAGGAC 573
Db 141 AGTCTCAAGGGCTCACCGCATGCGCATCTACTTCGCGGACGCCAAGGCCCTTCCCG 200
QY 574 ATCAGCCGACCGAGCGGCGCGCATGCTGATCCACATCGCGCGGCAACAGACCTGGT 633
Db 201 CTCGCGGCTCGGCATCGGCTCATCTCGAGCTCGGCGGACCGAGCTGTCGCCAGC 260
QY 634 AGCACCAGCGGTGGAAGAGCCCTGAGCTCGGCGTGACCAAGCTGGTGGAGCGTGG 693
Db 261 CTCGCGGCAAGCGCTCCAAAGCGCGCACTGGGTTCGGGATACGTCAGGCCCTACTAT 320
QY 694 ATCAGCGTGGCGGTGCGGAGACCCCACTACCTGTTCTGCGGCGTGCGGCAAG 753
Db 321 CCGGGGTGAACATCAAGTATCATCGCGCGGCAACAGAGTTCCTGGGGCGGACACG 380
QY 754 AACCGCGTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
Db 381 AACATCGTCCGCGCATACGAACTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
QY 814 TTCAGGCGCACCGCGCTGATCTACGCGCGCAAGACGACAGCGGCTGACGCTG 873
Db 441 ATCAAGGTGTCACCTCGATCGGTTGACGCGGTGACCAACACCTTCCGCGCTTCAAC 500
QY 874 GCCTGGAGCGCACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 933
Db 501 GCGGTGTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 560
QY 934 AGCATCCCCAGATCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 993
Db 561 CCGCTGCTGGCGCAAGGTGATCCCTACTTCCCTACAGGACACCGCGGCGGATCCAG 620
QY 994 ATCCGCAACTGGACAGGAGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1046
Db 621 CTGAACCTACGCGAGCTTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 673

RESULT 13
BI949774
LOCUS
DEFINITION
BI949774 852 bp mRNA linear EST 19-OCT-2001
HVSME10015024f Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME10015024f, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
AUTHORS
1. (bases 1 to 852)
Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen
S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
D.
TITLE
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
JOURNAL
COMMENT
Unpublished
Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 560
Seq primer: AATTAACTTCACTAAAGGG
High quality sequence stop: 735.
Location/Qualifiers
1. 852
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultiivar="Morex"
/db_xref="taxon:112509"
/clone="HVSME10015024f"
/tissue_type="Spike"
/lab_host="TJC121"
/clone_lib="Hordeum vulgare spike EST library HVCDNA0012"
(Fusarium infected)
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 163 a 311 c 262 g 113 t 3 others
ORIGIN

Query Match 7.1%; Score 74.4; DB 12; Length 852;
Best Local Similarity 47.4%; Pred. No. 0.00087;
Matches 222; Conservative 0; Mismatches 246; Indels 0; Gaps 0;
QY 579 CCGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 638
Db 57 CCGCAACTCGGCGATCGGCGCTCATCTCGACATCGGCAACGACGCTCGCCACATCGC 116
QY 639 CGCGCGGCTGGAGAAGCGCCTGAGCCTCGGCGGTGACCAAGCTGCTGAGCGCTGATCAG 698
Db 117 CGCAGACCTCAACGCGGCGCTCTCTGGGTCCAGAACAACTGTCGGCGCCCTTACCTGTC 176
QY 699 CGTGAAGCATCAAGTATACATCGCGCGGCAACGAGGTGCGAGGCGGCGGCGGCGGCGG 758
Db 177 CGTGAACATCAAGTATACATCGCGCGGCAACGAGGTGCGAGGCGGCGGCGGCGGCGGCGG 236
QY 759 CGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 818
Db 237 CCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 296
QY 819 GGCACCCACCGCGCTGATCTAGCGGCCCAAGGACGACGCGGCGGCGGCGGCGGCGGCGG 878
Db 297 GGTGTCACCTCATCCGCTTCAAGAGGTGGCCAACTCTTCCCGCGCCCTCCCGCGCGGT 356


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QY 879 GAGCGGCCACAGCGCCGCGTGGCGCGCCGCGGACATGCGCGCGCGCGTGGAGCAT 938
Db 357 GTTCAAGAAACCCCTACATGACGAGCTGGCCCGGCTCTGCGGAGACACCGCGCGCGCT 416
QY 939 CCCGAGATCATGACGCGCGCGCTGGACCAACGTTGAACATCGTGATGAATACATCCG 998
Db 417 GCTGGCCAAAGCTTACCCCTACTTTCGCGTACCGTGACAAACCCCGGAGCATCAGCCTGAA 476
QY 999 CAACCTGGACGAGACCGCGCGCATGTTGGCTCTGCGGAGACCG 1046
Db 477 CTACGCGACGTTCCAGCGCGGACACCGCGTGGTACCAACAAACCG 524

RESULT 14
BF261766 854 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEA0002C17f Hordeum vulgare seedling green leaf EST library
            cDNA clone HV_CEA0002C17f, mRNA sequence.
ACCESSION BF261766
VERSION BF261766.2 GI:13259943
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
          ; Triticeae; Hordeum.
REFERENCE 1. (bases 1 to 854)
          Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
          Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
          ,D.W., Fenton,R.D., Oates,R. and Main,D.
          Development of a genetically and physically anchored EST resource
          for barley genomics: Blumeria infected incompatible (Mla13)
          seedling leaf cDNA library
          Unpublished
          On Nov 17, 2000 this sequence version replaced gi:11192753.
          Contact: Wing RA
          Clemson University Genomics Institute
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Total hg bases = 509
          Seq primer: AATTACCTCACTAAAGGG
          High quality sequence stop: 727.
          Location/Qualifiers
            1..854
              /organism="Hordeum vulgare subsp. vulgare"
              /mol_type="mRNA"
              /cultivar="Cil16155 (Mla13)"
              /db_xref="taxon:112509"
              /clone="HV_CEA0002C17f"
              /tissue_type="seedling green leaf"
              /lab_host="TJC121"
              /clone_lib="Hordeum vulgare seedling green leaf EST
              library HVCDA0004 (Blumeria challenged)"
              /notes="vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
              C.I. 16155 (Mla13) plants were greenhouse grown in the R
              Wise lab at Iowa State University, Ames, IA; 7 day old
              green seedlings were challenged with isolate A27 (AvrMla13
              ) of Blumeria graminis f. sp. hordei, and leaves were
              harvested 20 and 24 hr post-inoculation and snap frozen;
              uninoculated leaves were harvested 20 hr post-inoculation
              (Wei, Wise). In the TJ Close lab at the University of
              California, Riverside, total RNA was prepared from each
              sample pool, equal quantities of all three RNA pools were
              combined, poly(A) RNA was purified from the mixture, one
              cDNA library was made, and 1 million pfu were in vivo
              excised to give pBluescript SK(-) cDNA phagemids (Choi,
              Close). Phagemids were plated and picked at the Clemson
              University Genomics Institute (CUGI) (Begum, Palmer,
              Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

```

```

sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders/Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 151 a 304 c 249 g 149 t 1 others
ORIGIN

Query Match 7.1%; Score 74.4; DB 10; Length 854;
Best Local Similarity 47.4%; Pred. No. 0.00087;
Matches 222; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 579 CGCAGCGAGCGCGCGCATGCTGATCCACATCGCGCGGACCAAGACCTGTGTGAGCAC 638
Db 258 CCGCAACTCCGGCATCGGCTCATCTCCGACATCGGCAACGACGATCGCAACATCGC 317
QY 639 CGCGCGCGTGGAGAGGSCCTGAGCCTGGGCGTGACCAAGCTGTTGGAGCGCTGATCAG 698
Db 318 CGCAGACCTCCACGCGGCGCTCTGGGTCCAGAAACAGCTGCGGCGCTTACTACCGTGC 377
QY 699 CGTGAGCGCGTGGCGGACGACCCCAACTACTCTTCTGCCGCGTGGCAAGAACGG 758
Db 378 CGTGAACATCAAGTACATCGCGCGGCAACGAGGTGTCATGGCGGCGGCGGACGAGCAT 437
QY 759 CGTGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 818
Db 438 CTTGCGGCGCATGCGCAACCTCAACGCGGCGCTCTCGGCGGCGGCGGCGGCGGCGG 497
QY 819 GGCCACCCCGCGCTGATCTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 878
Db 498 GGTGTCACCTCCATCCGTTGACGAGGTGGCGCAACTCTTCCCGCGCTTCCCGCGCGCT 557
QY 879 GAGCGGCCACAGCGCGCGCGTGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGTGGAGCAT 938
Db 558 GTTCAAGAACGCGCTACATGACGAGACTGGCGCGGCTCTTGGGAGGACACCGCGCGCGCT 617
QY 939 CCCGAGATCATGACGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 998
Db 618 GCTGGCCAAAGCTTACCCCTACTTTCGCTACCGTGACAAACCCCGGAGCATCAGCCTGAA 677
QY 999 CAACCTGGACGAGACCGCGGCGCATGTTGGCGCTTCTGGAGGACGG 1046
Db 678 CTACGCGACGTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725

RESULT 15
BF2664057 676 bp DNA linear GSS 17-DEC-2002
DEFINITION pacs2-164_4528.y2 pacs2-164 Pseudomonas aeruginosa genomic clone
ACCESSION pacs2-164_4528, genomic survey sequence.
VERSION BF2664057
KEYWORDS BF2664057.1 GI:27189080
SOURCE GSS.
ORGANISM Pseudomonas aeruginosa
          Pseudomonas aeruginosa
          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
          Pseudomonadaceae; Pseudomonas.
          1 (bases 1 to 676)
REFERENCE Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
          Burns,J.L., Kaul,R. and Olsen,W.V.
          Whole-Genome-Sequence variation among multiple isolates of
          Pseudomonas aeruginosa library
          J. Bacteriol., (2002) In press
          Contact: Chris K. Raymond
          Genome Center
          University of Washington

```

Search completed: December 16, 2003, 03:41:48
Job time : 2673 secs